

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:55:26 ; Search time 22 Seconds

(without alignments)
1095.879 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391
Sequence: 1 MTELPAPLSTFQNAQMSDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2391	100.0	467	3	US-08-706-344C-30
2	2384	99.7	467	3	US-08-706-344C-2
3	2379	99.5	467	3	US-08-706-344C-32
4	2378	99.5	467	2	US-08-967-101-134
5	2378	99.5	467	2	US-08-952-541-134
6	2378	99.5	467	3	US-08-923-554A-10
7	2378	99.5	467	3	US-08-670-964-2
8	2378	99.5	467	3	US-08-888-077A-2
9	2378	99.5	467	3	US-09-124-698-134
10	2378	99.5	467	3	US-09-127-480-134
11	2378	99.5	467	3	US-08-486-841C-134
12	2378	99.5	467	4	US-08-832-867-3
13	2378	99.5	467	4	US-08-227-725A-1
14	2378	99.5	467	4	US-09-124-523-134
15	2378	99.5	467	4	US-09-375-318-3
16	2378	99.5	467	4	US-09-636-796A-134
17	2378	99.3	467	4	US-08-706-344C-4
18	2372	99.2	467	2	US-08-967-101-2
19	2372	99.2	467	2	US-08-592-541-2
20	2372	99.2	467	2	US-09-124-698-2
21	2372	99.2	467	3	US-09-127-480-2
22	2372	99.2	467	3	US-08-496-841C-2
23	2372	99.2	467	3	US-08-706-344C-28
24	2372	99.2	467	4	US-09-124-523-2
25	2372	99.2	467	4	US-09-636-796A-2
26	2372	99.2	467	4	US-08-431-048F-2
27	2368	99.0	467	4	US-09-896-621B-4

28	2366	99.0	467	4	US-09-896-621B-5	Sequence 5, Appli
29	2356	98.5	467	4	US-09-896-621B-6	Sequence 6, Appli
30	2348	98.2	463	3	US-08-670-964-4	Sequence 4, Appli
31	2342	98.0	463	3	US-08-888-077A-4	Sequence 4, Appli
32	2333	97.6	463	4	US-08-937-834-6	Sequence 6, Appli
33	2325	97.2	463	2	US-08-670-479-18	Sequence 15, Appli
34	2291	95.8	462	3	US-08-788-231A-15	Sequence 15, Appli
35	2288	95.2	467	3	US-08-888-077A-17	Sequence 17, Appli
36	2228	93.2	467	3	US-08-496-841C-136	Sequence 136, App
37	2178	91.1	467	2	US-08-967-101-4	Sequence 4, Appli
38	2178	91.1	467	2	US-08-592-541-4	Sequence 4, Appli
39	2178	91.1	467	3	US-09-124-698-4	Sequence 4, Appli
40	2178	91.1	467	3	US-09-127-480-4	Sequence 4, Appli
41	2178	91.1	467	3	US-08-496-841C-4	Sequence 4, Appli
42	2178	91.1	467	4	US-09-124-523-4	Sequence 4, Appli
43	2178	91.1	467	4	US-09-636-796A-4	Sequence 4, Appli
44	2178	91.1	467	4	US-08-431-048F-4	Sequence 4, Appli
45	2174.5	90.9	465	3	US-08-788-231A-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-706-344C-30
; Sequence 30, Application US/08706344C
; Patent No. 6248555
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; APPLICANT: WASCO, WILLIAM
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; TITLE OF INVENTION: Alzheimer's Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,344C
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/003,054
; FILING DATE: 31-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0609.4180001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2640
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-706-344C-30

Query Match 100.0%; Score 2391; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-234;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MTELPAPLSTFQNAQMSDNLSNTVRSQNNRREQENDRSLGHPPLSGRPGQNSR 60
|||||

DB 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPEPLNSGRPOGNSR 60

QY 61 QVVEODEEDELTLTKYGAHVIMLFVPTLCMVVVAATIKSVSFYTRKQGLIYTPFTE 120

DB 61 QVVEODEEDELTLTKYGAHVIMLFVPTLCMVVVAATIKSVSFYTRKQGLIYTPFTE 120

QY 121 DTEVQGRALHSILNAAIMISIVYVMTLLVLYKYRCYKTHAMLLISSLLFFPSFI 180

DB 121 DTEVQGRALHSILNAAIMISIVYVMTLLVLYKYRCYKTHAMLLISSLLFFPSFI 180

QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

DB 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

QY 241 LPBWTAMLLAVISYVDVAVALCKGPIRLMVTROENETLFPALISSTVMVLVNAE 300

DB 241 LPBWTAMLLAVISYVDVAVALCKGPIRLMVTROENETLFPALISSTVMVLVNAE 300

QY 301 GDEPQRVRYSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

DB 301 GDEPQRVRYSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

QY 361 VOELSSSILAGDPEERGVKGLGDFIFYSYLVGKASATAGDMMTTIACFVALIIGLCL 420

DB 361 VOELSSSILAGDPEERGVKGLGDFIFYSYLVGKASATAGDMMTTIACFVALIIGLCL 420

QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVPFMDQLAFHQFYI 467

DB 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVPFMDQLAFHQFYI 467

RESULT 2

US-08-706-344C-2

Sequence 2, Application US/08706344C

Patent No. 6248555

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

APPLICANT: MASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial

TITLE OF INVENTION: Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,344C

FILING DATE: 30-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-706-344C-2

Query Match 99.7%; Score 2384; DB 3; Length 467;

Best Local Similarity 99.8%; Pred. No. 5,5e-234;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPEPLNSGRPOGNSR 60

DB 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPEPLNSGRPOGNSR 60

QY 61 QVVEODEEDELTLTKYGAHVIMLFVPTLCMVVVAATIKSVSFYTRKQGLIYTPFTE 120

DB 61 QVVEODEEDELTLTKYGAHVIMLFVPTLCMVVVAATIKSVSFYTRKQGLIYTPFTE 120

QY 121 DTEVQGRALHSILNAAIMISIVYVMTLLVLYKYRCYKTHAMLLISSLLFFPSFI 180

DB 121 DTEVQGRALHSILNAAIMISIVYVMTLLVLYKYRCYKTHAMLLISSLLFFPSFI 180

QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

DB 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

QY 241 LPBWTAMLLAVISYVDVAVALCKGPIRLMVTROENETLFPALISSTVMVLVNAE 300

DB 241 LPBWTAMLLAVISYVDVAVALCKGPIRLMVTROENETLFPALISSTVMVLVNAE 300

QY 301 GDEPQRVRYSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

DB 301 GDEPQRVRYSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

QY 361 VOELSSSILAGDPEERGVKGLGDFIFYSYLVGKASATAGDMMTTIACFVALIIGLCL 420

DB 361 VOELSSSILAGDPEERGVKGLGDFIFYSYLVGKASATAGDMMTTIACFVALIIGLCL 420

QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVPFMDQLAFHQFYI 467

DB 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVPFMDQLAFHQFYI 467

RESULT 3

US-08-706-344C-32

Sequence 32, Application US/08706344C

Patent No. 6248555

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

APPLICANT: MASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial

TITLE OF INVENTION: Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,344C

FILING DATE: 30-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-344C-32

Query Match 99.5%; Score 2379; DB 3; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.8e-233;
Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
QY 61 QVVEQDEEDELTLKYGAKVIMLFVPTLCMVVVAATIKSVSPYTRKDGQILYTPTE 120
DB 61 QVVEQDEEDELTLKYGAKVIMLFVPTLCMVVVAATIKSVSPYTRKDGQILYTPTE 120
QY 121 DTEYVQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
DB 121 DTEYVQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
QY 181 YIGEVFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKY 240
DB 181 YIGEVFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKY 240
QY 241 LPEWTAMLIAVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIIYSTWVLVNMAL 300
DB 241 LPEWTAMLIAVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIIYSTWVLVNMAL 300
QY 301 GPPEAQRKRSKSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
DB 301 GPPEAQRKRSKSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFAVAILGLCL 420
DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFAVAILGLCL 420
QY 421 TLLLLAIFKALPALPISITFGVFPATDYVQPFMDLAFHQFYI 467
DB 421 TLLLLAIFKALPALPISITFGVFPATDYVQPFMDLAFHQFYI 467

RESULT 4

US-08-967-101-134
Sequence 134, Application US/08967101
Patent No. 5860540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997

Carlson

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-101-134

Query Match 99.5%; Score 2378; DB 2; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
QY 61 QVVEQDEEDELTLKYGAKVIMLFVPTLCMVVVAATIKSVSPYTRKDGQILYTPTE 120
DB 61 QVVEQDEEDELTLKYGAKVIMLFVPTLCMVVVAATIKSVSPYTRKDGQILYTPTE 120
QY 121 DTEYVQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
DB 121 DTEYVQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
QY 181 YIGEVFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKY 240
DB 181 YIGEVFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKY 240
QY 241 LPEWTAMLIAVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIIYSTWVLVNMAL 300
DB 241 LPEWTAMLIAVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIIYSTWVLVNMAL 300
QY 301 GPPEAQRKRSKSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
DB 301 GPPEAQRKRSKSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFAVAILGLCL 420
DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFAVAILGLCL 420
QY 421 TLLLLAIFKALPALPISITFGVFPATDYVQPFMDLAFHQFYI 467
DB 421 TLLLLAIFKALPALPISITFGVFPATDYVQPFMDLAFHQFYI 467

RESULT 5

US-08-592-541-134
Sequence 134, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

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Fri Apr 9 06:19:30 2004

us-09-785-474a-30.ra1

Page 5

Db 421 TLLLAIFKALPALPISITFGVFPATDYVQPFMDQLAFHQFYI 467

RESULT 7

US-08-670-964-2

Sequence 2, Application US/08670964

Patent No. 6010874

GENERAL INFORMATION:

APPLICANT: Haidy, John A.

TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE

TITLE OF INVENTION: GENE AND GENE PRODUCTS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road - UW2220; P.O. Box 15

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/670,964

FILING DATE: 26-JUN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/001,142

FILING DATE: 13-JUL-1995

APPLICATION NUMBER: 60/001,501

FILING DATE: 18-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Han, William T

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: P0356

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-670-964-2

Query Match 99.5%; Score 2378; DB 3; Length 467;

Best Local Similarity 99.6%; Pred. No. 2.2e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MTELPAPLSYFQNAQMSNDNHLNNTVRSQNDNREROEHNDRLSGHPEPLSNGRPQNSR 60

QY 61 QVVEDEDEDEDELTKYGAHVIMLFPVTLQVWVVAITIKSVSFYTRKDGOLITPFTPE 120

Db 61 QVVEDEDEDEDELTKYGAHVIMLFPVTLQVWVVAITIKSVSFYTRKDGOLITPFTPE 120

QY 121 DTEYVQGRALHSILNAAIMISYIVMTILLVLYKRCYKVIHAWLIISSILLFFPSFI 180

Db 121 DTEYVQGRALHSILNAAIMISYIVMTILLVLYKRCYKVIHAWLIISSILLFFPSFI 180

Q R 6000

Db 241 LPEWTAMILLAVISYVDLVAVLCPKGPLRMVETAQOEENETLFPALLIYSTWVLVNAE 300

QY 301 GDEAQRVRSKNSKNAESTERESODTVAENDDGGFSEWEAQRDSHIGPHRSTESRAA 360

Db 301 GDEAQRVRSKNSKNAESTERESODTVAENDDGGFSEWEAQRDSHIGPHRSTESRAA 360

QY 361 VOELSSSIIAGDEPBERGVKLGDPITFYSVLVGAASATASGDWTTTACFVAIIIGLCL 420

Db 361 VOELSSSIIAGDEPBERGVKLGDPITFYSVLVGAASATASGDWTTTACFVAIIIGLCL 420

QY 421 TLLLAIFKALPALPISITFGVFPATDYVQPFMDQLAFHQFYI 467

Db 421 TLLLAIFKALPALPISITFGVFPATDYVQPFMDQLAFHQFYI 467

RESULT 8

US-08-888-077A-2

Sequence 2, Application US/08888077A

Patent No. 6020143

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USBS THEREFOR.

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ & MENTLIK

STREET: 600 SOUTH AVENUE WEST

CITY: WESTFIELD

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,077A

FILING DATE: 03-JUL-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,541

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: PALISI, THOMAS M

REGISTRATION NUMBER: 36,629

REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 654-5000

TELEFAX: (908) 654-7866

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-888-077A-2

Query Match 99.5%; Score 2378; DB 3; Length 467;

Best Local Similarity 99.6%; Pred. No. 2.2e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MTELPAPLSYFQNAQMSNDNHLNNTVRSQNDNREROEHNDRLSGHPEPLSNGRPQNSR 60

QY 61 QVVEDEDEDEDELTKYGAHVIMLFPVTLQVWVVAITIKSVSFYTRKDGOLITPFTPE 120

Db 61 QVVEDEDEDEDELTKYGAHVIMLFPVTLQVWVVAITIKSVSFYTRKDGOLITPFTPE 120

Carlen

DB 121 DTEVQGRALHSILNAIMSVYVMTILLVLYKRCYKHAMLLISLLFFPSFI 180
QY 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLRLOQAYLIMISALMALVFICY 240
DB 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLRLOQAYLIMISALMALVFICY 240
QY 241 LPEWTAMLLIAVISYVDLVAVLCLKGRLMLVETAOERNETLPPALISSITWMLVMAE 300
DB 241 LPEWTAMLLIAVISYVDLVAVLCLKGRLMLVETAOERNETLPPALISSITWMLVMAE 300
QY 301 GDEPAORRVSXNSKHNAESTERESQDTVAENDDGFSEMEAOERDHLGHRSTPESRAA 360
DB 301 GDEPAORRVSXNSKHNAESTERESQDTVAENDDGFSEMEAOERDHLGHRSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
QY 421 TLLLLAFKKALPALPISITFGVFEVPAFDYLVOPMDOLAFHOFYI 467
DB 421 TLLLLAFKKALPALPISITFGVFEVPAFDYLVOPMDOLAFHOFYI 467

RESULT 9

US-09-124-698-134
Sequence 134, Application US/09124698
Patent No. 611978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBAUT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-09-124-698-134

Query March 99.5%, Score 2378; DB 3; Length 467;
Best Local Similarity 99.6%, Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTFQNAQMSDNHLSNTVRSQNDNREROZHNDRSLGHEPPLSNRPOGNSR 60

DB 1 MTELPAPLSTFQNAQMSDNHLSNTVRSQNDNREROZHNDRSLGHEPPLSNRPOGNSR 60
QY 61 QVSEDEDEBELTKAGAHVIMLFVPTLQWVAVATIKSVSFYTRKDQOLIYPTFE 120
DB 61 QVSEDEDEBELTKAGAHVIMLFVPTLQWVAVATIKSVSFYTRKDQOLIYPTFE 120
QY 121 DTEVQGRALHSILNAIMSVYVMTILLVLYKRCYKHAMLLISLLFFPSFI 180
DB 121 DTEVQGRALHSILNAIMSVYVMTILLVLYKRCYKHAMLLISLLFFPSFI 180
QY 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLRLOQAYLIMISALMALVFICY 240
DB 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLRLOQAYLIMISALMALVFICY 240
QY 241 LPEWTAMLLIAVISYVDLVAVLCLKGRLMLVETAOERNETLPPALISSITWMLVMAE 300
DB 241 LPEWTAMLLIAVISYVDLVAVLCLKGRLMLVETAOERNETLPPALISSITWMLVMAE 300
QY 301 GDEPAORRVSXNSKHNAESTERESQDTVAENDDGFSEMEAOERDHLGHRSTPESRAA 360
DB 301 GDEPAORRVSXNSKHNAESTERESQDTVAENDDGFSEMEAOERDHLGHRSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
QY 421 TLLLLAFKKALPALPISITFGVFEVPAFDYLVOPMDOLAFHOFYI 467
DB 421 TLLLLAFKKALPALPISITFGVFEVPAFDYLVOPMDOLAFHOFYI 467

RESULT 10

US-09-127-480-134
Sequence 134, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBAUT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Protein
US-09-127-480-134

Query Match 99.5%; Score 2378; DB 3; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTRVRSQNDNREORHNDRLSGHPPLSNRPGQNSR 60
DB 1 MTELPAPLSYFQNAQMSDNHLSNTRVRSQNDNREORHNDRLSGHPPLSNRPGQNSR 60
QY 61 QVEODEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRKDGQLIYTPETE 120
DB 61 QVEODEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRKDGQLIYTPETE 120
QY 121 DTEVGGRAHSLINAAIMISVIVMTLLVLYKRCYKVIHAWLIISSLLFFFSFI 180
DB 121 DTEVGGRAHSLINAAIMISVIVMTLLVLYKRCYKVIHAWLIISSLLFFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHKGPLRQQAIVIMISALMALVFIKY 240
DB 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHKGPLRQQAIVIMISALMALVFIKY 240
QY 241 LPEWTAMLLIAVSYVDVAVLCCKPLRMVETLQERNETLFPALIIYSTWMLVNMAR 300
DB 241 LPEWTAMLLIAVSYVDVAVLCCKPLRMVETLQERNETLFPALIIYSTWMLVNMAR 300
QY 301 GDEPQRRVSKSKNAESTERESODTVANDDGFSSEWEAQRDHLGPHRSTPESRAA 360
DB 301 GDEPQRRVSKSKNAESTERESODTVANDDGFSSEWEAQRDHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQDLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQDLAFHQFYI 467

RESULT 11

US-08-496-841C-134
Sequence 134, Application US/08496841C
Patent No. 6210939

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSES: Darby & Darby, PC

CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C

FILING DATE: 28-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 134

US-08-496-841C-134

Query Match 99.5%; Score 2378; DB 3; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTRVRSQNDNREORHNDRLSGHPPLSNRPGQNSR 60
DB 1 MTELPAPLSYFQNAQMSDNHLSNTRVRSQNDNREORHNDRLSGHPPLSNRPGQNSR 60
QY 61 QVEODEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRKDGQLIYTPETE 120
DB 61 QVEODEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRKDGQLIYTPETE 120
QY 121 DTEVGGRAHSLINAAIMISVIVMTLLVLYKRCYKVIHAWLIISSLLFFFSFI 180
DB 121 DTEVGGRAHSLINAAIMISVIVMTLLVLYKRCYKVIHAWLIISSLLFFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHKGPLRQQAIVIMISALMALVFIKY 240
DB 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHKGPLRQQAIVIMISALMALVFIKY 240
QY 241 LPEWTAMLLIAVSYVDVAVLCCKPLRMVETLQERNETLFPALIIYSTWMLVNMAR 300
DB 241 LPEWTAMLLIAVSYVDVAVLCCKPLRMVETLQERNETLFPALIIYSTWMLVNMAR 300
QY 301 GDEPQRRVSKSKNAESTERESODTVANDDGFSSEWEAQRDHLGPHRSTPESRAA 360
DB 301 GDEPQRRVSKSKNAESTERESODTVANDDGFSSEWEAQRDHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQDLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQDLAFHQFYI 467

RESULT 12

US-08-832-867-3
Sequence 3, Application US/08832867C
Patent No. 6376239

GENERAL INFORMATION:
APPLICANT: BAUMEISTER, Ralf

TITLE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF
CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN
TITLE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.
TITLE OF INVENTION: ELEGANS AND USES THEREOF
FILE REFERENCE: 674503-2004
CURRENT APPLICATION NUMBER: US/08/832,867C
CURRENT FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
LENGTH: 467
TYPE: PRT

ORGANISM: Caenorhabditis elegans
US-08-832-867-3

Query Match 99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSYFQNAQMSDNHLSNTRVRSQNDNREORHNDRLSGHPPLSNRPGQNSR 60

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Db      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60
Qy      61 QVEEDDEDEDELTLYKGAHVIMLFVPTLCMVVVAITIKSVFTRKQGLIYTPPTE 120
Db      61 QVEEDDEDEDELTLYKGAHVIMLFVPTLCMVVVAITIKSVFTRKQGLIYTPPTE 120
Qy      121 DTEVQGRALHSILNAINMSIVVMTILLVLYKRCYKVIHAWLIISSLLLPFFSFI 180
Db      121 DTEVQGRALHSILNAINMSIVVMTILLVLYKRCYKVIHAWLIISSLLLPFFSFI 180
Qy      181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLQOAVYIMTSALMALVFIKY 240
Db      181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLQOAVYIMTSALMALVFIKY 240
Qy      241 LPEWTAMLIAVISVDLVAVLCLKGPLRLMVEAQRNETLFPALIIYSTMWLVNMAE 300
Db      241 LPEWTAMLIAVISVDLVAVLCLKGPLRLMVEAQRNETLFPALIIYSTMWLVNMAE 300
Qy      301 GDEPAQRVSKNSKNNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
Db      301 GDEPAQRVSKNSKNNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
Qy      361 VOELSSSTILAGEDEBERGVKLGDPFIYSVLVKGASATASGDMNTTIACFVALILGLCL 420
Db      361 VOELSSSTILAGEDEBERGVKLGDPFIYSVLVKGASATASGDMNTTIACFVALILGLCL 420
Qy      421 TLILLAIFFKALPALPISITFGLVFYATDYLVOFPMDOIAFHOFYI 467
Db      421 TLILLAIFFKALPALPISITFGLVFYATDYLVOFPMDOIAFHOFYI 467

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RESULT 13

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US-09-227-725A-1
; Sequence 1, Application US/09227725A
; Patent No. 6383758
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Rommens, Johanna
; APPLICANT: Fraser, Paul E.
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; TITLE OF INVENTION: Of Use
; FILE REFERENCE: 1034/1F810-US1
; CURRENT APPLICATION NUMBER: US/09/227,725A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-227-725A-1

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Query Match      99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60
Qy      61 QVEEDDEDEDELTLYKGAHVIMLFVPTLCMVVVAITIKSVFTRKQGLIYTPPTE 120
Db      61 QVEEDDEDEDELTLYKGAHVIMLFVPTLCMVVVAITIKSVFTRKQGLIYTPPTE 120
Qy      121 DTEVQGRALHSILNAINMSIVVMTILLVLYKRCYKVIHAWLIISSLLLPFFSFI 180
Db      121 DTEVQGRALHSILNAINMSIVVMTILLVLYKRCYKVIHAWLIISSLLLPFFSFI 180
Qy      181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLQOAVYIMTSALMALVFIKY 240
Db      181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLQOAVYIMTSALMALVFIKY 240

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Qy      241 LPEWTAMLIAVISVDLVAVLCLKGPLRLMVEAQRNETLFPALIIYSTMWLVNMAE 300
Db      241 LPEWTAMLIAVISVDLVAVLCLKGPLRLMVEAQRNETLFPALIIYSTMWLVNMAE 300
Qy      301 GDEPAQRVSKNSKNNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
Db      301 GDEPAQRVSKNSKNNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
Qy      361 VOELSSSTILAGEDEBERGVKLGDPFIYSVLVKGASATASGDMNTTIACFVALILGLCL 420
Db      361 VOELSSSTILAGEDEBERGVKLGDPFIYSVLVKGASATASGDMNTTIACFVALILGLCL 420
Qy      421 TLILLAIFFKALPALPISITFGLVFYATDYLVOFPMDOIAFHOFYI 467
Db      421 TLILLAIFFKALPALPISITFGLVFYATDYLVOFPMDOIAFHOFYI 467

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RESULT 14

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US-09-124-523-134
; Sequence 134, Application US/09124523
; Patent No. 6393960
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-124-523-134

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Query Match      99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60
Qy      61 QVEEDDEDEDELTLYKGAHVIMLFVPTLCMVVVAITIKSVFTRKQGLIYTPPTE 120
Db      61 QVEEDDEDEDELTLYKGAHVIMLFVPTLCMVVVAITIKSVFTRKQGLIYTPPTE 120

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QY 121 DTEVGQRALHSILNAAIMISVIVVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVGQRALHSILNAAIMISVIVVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLIMNFVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALLIMNFVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPBWTAMLILAVISYVDLVAVCLKGPLRLMVEVTAOERNETLFPALITYSTWVLVMAE 300
 DB 241 LPBWTAMLILAVISYVDLVAVCLKGPLRLMVEVTAOERNETLFPALITYSTWVLVMAE 300
 QY 301 GDEPAQRVSKSKNAESTERESODTYAENDDGFSEMEARQDSHIGPHRSTPESRAA 360
 DB 301 GDEPAQRVSKSKNAESTERESODTYAENDDGFSEMEARQDSHIGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 QY 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467
 DB 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467

RESULT 15

US-09-375-318-3
 Sequence 3, Application US/09375318
 Patent No. 6468791

GENERAL INFORMATION:

APPLICANT: Tenzi, Rudolph E.
 Schellenders, Gerard D.
 Masco, Wilma
 Levy-Ianad, Ephrat
 Bird, Thomas D.
 Galas, David J.
 TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
 ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESS: SEED and BEERY LLP
 STREET: 701 Fifth Ave, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/375,318
 FILING DATE: 16-Aug-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Verma, James M.
 REGISTRATION NUMBER: 33,287
 REFERENCE/DOCKET NUMBER: 920010.571C1
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-375-318-3

Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233;

Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTELPAPLSYFQNAQSEBNHLSNTVRSQNDREOEHNDRSLGHPFLSNGRQGNR 60
 DB 1 MTELPAPLSYFQNAQSEBNHLSNTVRSQNDREOEHNDRSLGHPFLSNGRQGNR 60
 QY 61 QVEQDEEEDDELTLYKGAHVIMLFVPTLCMVVVAITIKSVSFYTRDQGLIYPTFE 120
 DB 61 QVEQDEEEDDELTLYKGAHVIMLFVPTLCMVVVAITIKSVSFYTRDQGLIYPTFE 120
 QY 121 DTEVGQRALHSILNAAIMISVIVVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVGQRALHSILNAAIMISVIVVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLIMNFVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALLIMNFVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPBWTAMLILAVISYVDLVAVCLKGPLRLMVEVTAOERNETLFPALITYSTWVLVMAE 300
 DB 241 LPBWTAMLILAVISYVDLVAVCLKGPLRLMVEVTAOERNETLFPALITYSTWVLVMAE 300
 QY 301 GDEPAQRVSKSKNAESTERESODTYAENDDGFSEMEARQDSHIGPHRSTPESRAA 360
 DB 301 GDEPAQRVSKSKNAESTERESODTYAENDDGFSEMEARQDSHIGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 QY 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467
 DB 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467

Search completed: April 8, 2004, 16:59:19
 Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:54:31 ; Search time 21 Seconds

(without alignments)
2139.116 Million cell updates/sec

Title: US-09-785-474a-30

Perfect score: 2391
Sequence: 1 MTELPAPLSTYFQNAQMSDNL.....ATDYLQPMQDLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Dirl:*
2: Dirl:*
3: Dirl:*
4: Dirl:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2378	99.5	467	2 S58396	presenilin 1, sp1
2	2348	98.2	463	2 S53683	presenilin 1-463
3	2266	94.8	467	2 UC5080	presenilin 1 prote
4	2236	93.5	463	2 UC5081	presenilin 1 prote
5	2228	93.2	467	2 J78388	5182 protein - mou
6	1801	75.3	433	2 UC5390	presenilin-alpha
7	1584	66.2	374	2 S63684	presenilin 1, sp1
8	1462.5	61.2	449	2 UC5391	presenilin-beta
9	1444	60.4	448	2 A56993	presenilin 2 - hum
10	1376.5	57.6	442	2 J39174	seven trans-membra
11	1054.5	44.1	836	2 B89453	protein F35H12.3 l
12	963.5	40.3	461	2 S60253	se1-12 protein - C
13	539.5	22.6	453	2 T00724	presenilin homolog
14	538	22.5	397	2 A84702	probable presenili
15	505	21.1	358	2 T15184	presenilin-beta ho
16	309.5	12.9	465	2 T77885	sperm membrane pro
17	122.5	5.5	455	2 H97237	membrane associate
18	120.5	5.0	2386	2 T39911	rad3 checkpoint pr
19	118.5	5.0	309	2 H90548	hypothetical prote
20	117	4.9	601	2 S12004	tyramine receptor
21	115	4.8	364	2 D95959	conserved hypochet
22	115	4.8	601	2 JH0170	octopamine recepto
23	114.5	4.8	323	2 A48997	tumor surface anti
24	111.5	4.7	339	2 CT1132	hypothetical prote
25	110	4.6	318	2 B84291	hypothetical prote
26	110	4.6	707	2 T09340	hypothetical prote
27	109.5	4.6	598	2 T05130	hypothetical prote
28	109	4.6	599	2 T24333	hypothetical prote
29	108.5	4.5	887	2 S73768	Mo277 homolog Fl1

ALIGNMENTS

RESULT 1

S58396

presenilin 1, splice form 467 - human

C/Species: Homo sapiens (man)

C/Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999

C/Accession: S58396; S71401; S71402

R/Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Chi

ero, I.; Pinessi, L.; Nee, L.; Chinnakov, I.; Pollen, D.; Brookes, A.; Sansau, P.; Polj

E.; Rommens, J.M.; St George-Hyslop, P.H.

Nature 375, 754-760, 1995

A/Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer

A/Reference number: 158095; PMID:95319502; PMID:7596406

A/Accession: S58396

A/Molecule type: mRNA

A/Residues: 1-467 <SHE>

A/Cross-references: EMBL:142110; NID:9904118; PIRN:AB46416.1; PID:9904119

R/Idal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.

FEBS Lett. 393, 19-23, 1996

A/Title: Alzheimer's presenilin 1 gene expression in platelets and megakaryocytes. Ider

A/Reference number: S71401; PMID:96397521; PMID:8804415

A/Accession: S71401

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 24-32/254-256,290-292/316-317,376-379 <YIM>

A/Experimental source: Dani megakaryotic cell line (ATCC CRL-9792) and platelets

C/Genetics: A/Gene: GDB:PSEN1; AD3; FAD; S182; PS1

A/Cross-references: GDB:135682; OMIM:104311

A/Map position: 14q24.3-14q24.3

C/Suprafamily: presenilin

F/82-100/Domain: transmembrane #status predicted <TM1>

F/133-154/Domain: transmembrane #status predicted <TM2>

F/164-185/Domain: transmembrane #status predicted <TM3>

F/195-213/Domain: transmembrane #status predicted <TM4>

F/221-238/Domain: transmembrane #status predicted <TM5>

F/244-264/Domain: transmembrane #status predicted <TM6>

F/281-301/Domain: transmembrane #status predicted <TM7>

F/406-426/Domain: transmembrane #status predicted <TM8>

F/433-453/Domain: transmembrane #status predicted <TM9>

F/479-405/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best local similarity 99.6%; Pred. No. 1.3e-17;

Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSDNLSTVRSQNDKRENDNRSLGHPPLSGRQGNR 60

DB 1 MTELPAPLSTYFQNAQMSDNLSTVRSQNDKRENDNRSLGHPPLSGRQGNR 60

QY 61 QVVEDEDEDEDETLKYGAKHVMLEFVTLQMVVVATIXSVSFYTRKQGLIYPTFE 120

```

Db      61 QVEQDEDEBELTLTKGAGHVMLEFVTLICMNVVATIKSVFTRKDGQILYPTFE 120
Qy      121 DTEVQGRALHSILNAAIMISVIVMTILLVLYKRCYKVIHAMLIISSLLILFFPSFI 180
      121 DTEVQGRALHSILNAAIMISVIVMTILLVLYKRCYKVIHAMLIISSLLILFFPSFI 180
Qy      181 YLGEVEKTYNVAVDYITVALLINMGVGMISIMHGKPLRLOQAYLIMISALMAVFIKY 240
      181 YLGEVEKTYNVAVDYITVALLINMGVGMISIMHGKPLRLOQAYLIMISALMAVFIKY 240
Db      241 LPEWTAMLILAVISYVDLVAVLCLKGPLRMLVETAOERNETLPPALIIYSTWMLVNMAS 300
      241 LPEWTAMLILAVISYVDLVAVLCLKGPLRMLVETAOERNETLPPALIIYSTWMLVNMAS 300
Qy      301 GDPBAQRVSKNSKHNASTRESQDTVAENDDGGFSEBEAQRDSHGLGHRSTPESRAA 360
      301 GDPBAQRVSKNSKHNASTRESQDTVAENDDGGFSEBEAQRDSHGLGHRSTPESRAA 360
Db      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420
      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420
Qy      421 TLLILAIKKALPALPISITFGLVFYFATDYLVOFPMDQLAFHOFYI 467
      421 TLLILAIKKALPALPISITFGLVFYFATDYLVOFPMDQLAFHOFYI 467

```

RESULT 2

663683
 presentin I-463 - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
 C:Accession: S63683
 R:Sahara, N.; Yabagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shtirasawa, T.; M
 FBS Letc. 381-7-11, 1996
 A:Title: Identification and characterization of presentin I-467, I-463 and I-374.
 A:Reference number: S63683; MUID:96193901; PMID:8641442
 A:Accession: S63683
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1463 <SAH>
 A:Cross-references: EMBL:U40379; NID:g1244637; PIDN:AA05894.1; PID:g1244638
 C:Superfamily: presentin

Query Match 98.2%; Score 2348; DB 2; Length 463;
 Best Local Similarity 98.7%; Pred. No. 2, 9e-175;
 Matches 461; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

```

Qy      1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDREOHNDRLSLGHPBLSNGRPOGNSR 60
      1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDREOHNDRLSLGHPBLSNGRPOGNSR 60
Db      61 QVEQDEDEBELTLTKGAGHVMLEFVTLICMNVVATIKSVFTRKDGQILYPTFE 120
      61 QVEQDEDEBELTLTKGAGHVMLEFVTLICMNVVATIKSVFTRKDGQILYPTFE 120
Qy      121 DTEVQGRALHSILNAAIMISVIVMTILLVLYKRCYKVIHAMLIISSLLILFFPSFI 180
      121 DTEVQGRALHSILNAAIMISVIVMTILLVLYKRCYKVIHAMLIISSLLILFFPSFI 180
Db      181 YLGEVEKTYNVAVDYITVALLINMGVGMISIMHGKPLRLOQAYLIMISALMAVFIKY 240
      181 YLGEVEKTYNVAVDYITVALLINMGVGMISIMHGKPLRLOQAYLIMISALMAVFIKY 240
Qy      241 LPEWTAMLILAVISYVDLVAVLCLKGPLRMLVETAOERNETLPPALIIYSTWMLVNMAS 300
      241 LPEWTAMLILAVISYVDLVAVLCLKGPLRMLVETAOERNETLPPALIIYSTWMLVNMAS 300
Db      301 GDPBAQRVSKNSKHNASTRESQDTVAENDDGGFSEBEAQRDSHGLGHRSTPESRAA 360
      301 GDPBAQRVSKNSKHNASTRESQDTVAENDDGGFSEBEAQRDSHGLGHRSTPESRAA 360
Qy      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420
      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420

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Qy      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420
      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 416
Qy      421 TLLILAIKKALPALPISITFGLVFYFATDYLVOFPMDQLAFHOFYI 467
      421 TLLILAIKKALPALPISITFGLVFYFATDYLVOFPMDQLAFHOFYI 463

```

RESULT 3

UCS080
 presentin 1 protein isoform 467 - lesser mouse lemur
 C:Species: Microcebus murinus (lesser mouse lemur)
 C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
 C:Accession: JCS080
 R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Peltier, A.; Bonn, N.; Belle
 Biochem. Biophys. Res. Commun. 228, 430-439, 1996
 A:Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene
 A:Reference number: JCS080; MUID:97079199; PMID:8920931
 A:Accession: JCS080
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1467 <CAL>
 A:Cross-references: EMBL:Z71333; NID:g1707591; PIDN:CA95930.1; PID:g1707592
 A:Experimental source: brain
 A:Comment: This protein is an integral membrane protein with seven transmembrane doma
 C:Genetics:
 A:Gene: pal
 A:Map position: 14
 C:Superfamily: presentin
 C:Keywords: transmembrane protein
 F:83-100/Domain: transmembrane #status predicted <TM1>
 F:133-154/Domain: transmembrane #status predicted <TM2>
 F:164-185/Domain: transmembrane #status predicted <TM3>
 F:195-213/Domain: transmembrane #status predicted <TM4>
 F:221-238/Domain: transmembrane #status predicted <TM5>
 F:244-261/Domain: transmembrane #status predicted <TM6>
 F:408-428/Domain: transmembrane #status predicted <TM7>

Query Match 94.8%; Score 2266; DB 2; Length 467;
 Best Local Similarity 94.6%; Pred. No. 7, 1e-169;
 Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

```

Qy      1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDREOHNDRLSLGHPBLSNGRPOGNSR 60
      1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDREOHNDRLSLGHPBLSNGRPOGNSG 60
Db      61 QVEQDEDEBELTLTKGAGHVMLEFVTLICMNVVATIKSVFTRKDGQILYPTFE 120
      61 PYVERDEDEBELTLTKGAGHVMLEFVTLICMNVVATIKSVFTRKDGQILYPTFE 120
Qy      121 DTEVQGRALHSILNAAIMISVIVMTILLVLYKRCYKVIHAMLIISSLLILFFPSFI 180
      121 DTEVQGRALHSILNAAIMISVIVMTILLVLYKRCYKVIHAMLIISSLLILFFPSFI 180
Db      181 YLGEVEKTYNVAVDYITVALLINMGVGMISIMHGKPLRLOQAYLIMISALMAVFIKY 240
      181 YLGEVEKTYNVAVDYITVALLINMGVGMISIMHGKPLRLOQAYLIMISALMAVFIKY 240
Qy      241 LPEWTAMLILAVISYVDLVAVLCLKGPLRMLVETAOERNETLPPALIIYSTWMLVNMAS 300
      241 LPEWTAMLILAVISYVDLVAVLCLKGPLRMLVETAOERNETLPPALIIYSTWMLVNMAS 300
Db      301 GDPBAQRVSKNSKHNASTRESQDTVAENDDGGFSEBEAQRDSHGLGHRSTPESRAA 360
      301 GDPBAQRVSKNSKHNASTRESQDTVAENDDGGFSEBEAQRDSHGLGHRSTPESRAA 360
Qy      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420
      361 VOELSSSIIAGEDEBERGVKLGIDFIYSVLVKASATASGDMNTTIACFVAILIGLCL 420

```

Db 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHQFYI 467

RESULT 4

JC5081

presentin 1 protein isoform 463 - lesser mouse lemur

C/Species: Microtus murinus (lesser mouse lemur)
C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C/Accession: JC5081

R/Calandra, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Pelter, A.; Bone, N.; Bellis,
Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A/Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene in
A/Reference number: JC5081; MUID:97079199; PMID:8920931

A/Contents: Brain

A/Accession: JC5081

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-463 <CAL>

A/Cross-references: EMBL:Z7133

A/Comment: This protein is an intermembrane protein with seven transmembrane domains. It

C/Genetics:

A/Gene: psl

A/Map position: 14

C/Superfamily: presentin

C/Keywords: transmembrane protein

F/78-96/Domain: transmembrane #status predicted <TM1>

F/129-150/Domain: transmembrane #status predicted <TM2>

F/160-181/Domain: transmembrane #status predicted <TM3>

F/191-209/Domain: transmembrane #status predicted <TM4>

F/212-234/Domain: transmembrane #status predicted <TM5>

F/240-257/Domain: transmembrane #status predicted <TM6>

F/404-424/Domain: transmembrane #status predicted <TM7>

Query Match 93.5%; Score 2236; DB 2; Length 463;
Best Local Similarity 93.8%; Pred. No. 1.5e-166;
Matches 438; Conservative 12; Mismatches 13; Indels 4; Gaps 1;

```

Qy 1 MTEIPAPLSYFQNAQMSNDNLNTVRSQNDNRERQENDRSLGHPPLSNGRPGNSR 60
Db 1 MTEIPAPLSYFQNAQMSNDNLNTVRSQNDNRERQENDRSLGHPPLSNGRPGNSG 56
Qy 61 QVEODEEEDDELTLYGAKAVIMLPVPTLCMVVVVATIKVSFPTKDGQLITPTE 120
Db 57 PVVERDEDEDELTLYGAKAVIMLPVPTLCMVVVVATIKVSFPTKDGQLITPTE 116
Qy 121 DTEVQGRALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLLISLLLEFFSFI 180
Db 117 DTEVQGRALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLLISLLLEFFSFI 176
Qy 181 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYKY 240
Db 177 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYKY 236
Qy 241 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERETLFPALISYSTMVLMNAE 300
Db 237 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERETLFPALISYSTMVLMNAE 296
Qy 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTESRAA 360
Db 297 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTESRAA 356
Qy 361 VOELSSSITLAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTITACFVAIIIGLCL 420
Db 357 VOELSSSITLAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTITACFVAIIIGLCL 416
Qy 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHQFYI 467
Db 417 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHQFYI 463

```

RESULT 5

I78388

S182 protein - mouse

C/Species: Mus musculus (house mouse)

C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999

C/Accession: I78388

R/Sherrington, R.; Rogae, E.; Liang, Y.; Rogae, E.A.; Levesque, G.; Ikeda, M.; Chi
ero, I.; Bines, L.; Nee, L.; Chumakov, I.; Follen, D.; Brookes, A.; Sasseau, P.; Polt
E.; Rommens, J.M.; St George-Hyslop, P.H.
Nature 375, 754-760, 1995

A/Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer
A/Reference number: I58095; MUID:95319502; PMID:7596406

A/Accession: I78388

A/Status: preliminary; translated from GB/EMBL/DDDJ

A/Molecule type: mRNA

A/Residues: 1-467 <RES>

A/Cross-references: GB:I42177; NID:9904129; PIDN:AAQ2094.1; PID:9904130

C/Superfamily: presentin

Query Match 93.2%; Score 2228; DB 2; Length 467;
Best Local Similarity 92.3%; Pred. No. 6.5e-166;
Matches 431; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

```

Qy 1 MTEIPAPLSYFQNAQMSNDNLNTVRSQNDNRERQENDRSLGHPPLSNGRPGNSR 60
Db 1 MTEIPAPLSYFQNAQMSNDNLNTVRSQNDNRERQENDRSLGHPPLSNGRPGNSR 60
Qy 61 QVEODEEEDDELTLYGAKAVIMLPVPTLCMVVVVATIKVSFPTKDGQLITPTE 120
Db 61 QVEODEEEDDELTLYGAKAVIMLPVPTLCMVVVVATIKVSFPTKDGQLITPTE 120
Qy 121 DTEVQGRALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLLISLLLEFFSFI 180
Db 121 DTEVQGRALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLLISLLLEFFSFI 180
Qy 181 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYKY 240
Db 181 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYKY 240
Qy 241 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERETLFPALISYSTMVLMNAE 300
Db 241 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERETLFPALISYSTMVLMNAE 300
Qy 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTESRAA 360
Db 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEMEARQDSHLGPHRSTESRAA 360
Qy 361 VOELSSSITLAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTITACFVAIIIGLCL 420
Db 361 VOELSSSITLAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTITACFVAIIIGLCL 420
Qy 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHQFYI 467
Db 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHQFYI 467

```

RESULT 6

JC5390

presentin-alpha - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C/Accession: JC5390

R/Tsujiyama, A.; Yasojima, K.; Hashimoto-Gotoh, T.

Biochem. Biophys. Res. Commun. 221, 392-396, 1997

A/Title: Cloning of Xenopus presentin-alpha and -beta cDNAs and their differential exp

A/Reference number: JC5390; MUID:97223465; PMID:9070286

A/Accession: JC5390

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-433 <TSU>

A/Cross-references: DDBJ:D84427; NID:91944353; PIDN:BAI9570.1; PID:91944354

A/Experimental source: brain

C/Comment: This protein plays a role in negative regulation of apoptotic cascades during

F/48-66/Domain: transmembrane #status predicted <TM1>

F/99-119/Domain: transmembrane #status predicted <TM2>

F:130-1149/Domain:	transmembrane	#status	predicted	<TM>
F:161-178/Domain:	transmembrane	#status	predicted	<TM>
F:187-203/Domain:	transmembrane	#status	predicted	<TM>
F:210-227/Domain:	transmembrane	#status	predicted	<TM>
F:374-394/Domain:	transmembrane	#status	predicted	<TM>

Query Match	75.3%	Score 1801	DB 2	Length 433
Best Local Similarity	82.8%	Pred. No. 1,1e-132		
Matches 355	Conservative 26	Mismatches 48	Indels 0	Gaps 0

Qy	39	NDRSLSGPEPPLSNRPOGNSROVAYODEEEDDEELTKYGAQHVTMLFVPTVLCAVVVYA	98
Dd	5	SERBNENSESQSNQOTQSSSQVLEODEBEDEELTKYGAQHVTMLFVPTVLCAVVVYA	64
Qy	99	TIKVSFYTRKDQGLIYTPFTEDTETVGORALHSILNAIMISVIVMTILLVVLKYRC	158
Dd	65	TIKVSFYTRFDQGLIYTPFTEDTESVGORALNSILNATIMISVIVMTILLVVLKYRC	124
Qy	159	YKVJHAMILLSSLLFFFSFYLGVEVKYTNVADYITVALLNNPGVNGMISHMGCP	218
Dd	125	YKVJHGMILLSSLLFFFSFYLGVEVKYTNVADYITVALLNNFGVNGMISHMGCP	184
Qy	219	LRLQOAYIIMISALMALVFIKLPBEMTAMLLIAVISYVDLVAVLCKLPLMLVETAQER	278
Dd	165	LJLQOAYIIMISALMALVFIKLPBEMTAMLLIAVISYVDLVAVLSKPLMLVETAQER	244
Qy	279	NETLFPALIVYSTWVWLVNVAABDPEAQRVSKNSKNAESTERESQDTVAENDDGSE	338
Dd	245	NETLFPALIVYSTWVWLVNVAADGDFGLKQASHTKYVNCAPAHPRSDSASDDGSGFDT	304
Qy	339	EMELQRDCHLPHRSTPESRAAVOELSSILAGEDPEERGVYLGJGDDIFSVILVGRSA	398
Dd	305	TWEDHRNAQIGFIYSTPESRAVAQALPNSPSPGEPPEERGVYLGJGDDIFSVILVGRSA	364
Qy	399	TASGDMNTTICFAVAILGLCTILLLLAIFKKALPALDISIFGLVVFYFATDYLVQPFMD	458
Dd	365	TASGDMNTTICFAVAILGLCTILLLLAIFKKALPALDISIFGLVVFYFATDYLVQPFMD	424
Qy	459	QIAFHQFYI	467
Dd	425	QIAFHQFYI	433

RESULT 7
S63684
Presentin 1, splice form 374 - human
N:Alternative names: Alzheimer's disease protein 3
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C:Accession: S63684
R:Satoh, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shiraasawa, T.; I
FEBS Lett. 381, 7-11, 1996
A:Title: Identification and characterization of presentin I-467, I-463 and I-574.
A:Reference number: S63683; MUID:96193901; PMID:8641442
A:Accession: S63684
A:Status: Preliminary; nucleic acid sequence not shown
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-374 <SAs>
A:Cross-references: EMBL:U040380; NID:G1244639; FIDN:AAB05895.1; PID:G1244640
C:Genetics:
A:Gene: GDB:PSEN1, AD3, FAD, S182, PS1
A:Cross-references: GDB:135662; OMTW:104311
A:Map position: 14q24.3-14q24.3
A:Superfamily: presentin 1

```

Query March 56.2%; Score 1584; DB 2; Length 374;
Best Local Similarity 98.1%; Pzed 7.5e-116;
Matches 312; Conservative 1; Mismatches 1; Indels 4; Gaps 1

Cy 1 MTELPLPLSTFQNAQMSNDNLSTNTVRSQNDNRHREHNDNRSLGHDPEYLSNGRPGQNGR 60
    1 MTELPLPLSTFQNAQMSNDNLSTNTVRSQNDNRHREHNDNRSLGHDPEYLSNGRPGQNGR 56

```

Qy	6	QVVEQDEEBEELTLKYGKAHYIM.FVEVTLQMVVAATISVGFYRKOGLIYPFTE	120
Qy	57	QVVEQDEEBEELTLKYGKAHYIM.FVEVTLQMVVAATISVGFYRKOGLIYPFTE	116
Qy	121	DTETVQGRALHSLINAAIMISVIVMTLLVLVLYKRCYKIHAMLISSLLFFPSFI	180
Db	117	DTETVQGRALHSLINAAIMISVIVMTLLVLVLYKRCYKIHAMLISSLLFFPSFI	176
Qy	181	YLSEVKTNNVADVITYALLIMNFGVGMISIMKGPRLQCAYLIMISALMAVFIKY	240
Db	177	YLSEVKTNNVADVITYALLIMNFGVGMISIMKGPRLQCAYLIMISALMAVFIKY	236
Qy	241	LPENTAMILLIAVISYVDLVAVLCLXGPLRMLVETAOEBNETLFPALLIYSTMWLVNMAE	300
Db	237	LPENTAMILLIAVISYVDLVAVLCPXGPLRMLVETAOEBNETLFPALLIYSTMWLVNMAE	296
Qy	301	GDEPAQRVSKNSKINAAE 318	
Db	297	GDEPAQRVSKNSKINAAE 314	

RESULT 8
JC5391
presentinlin-beta - African clawed frog
CISpecies: Xenopus laevis (African clawed frog)
CIDate: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
CAccession: JC5391
RITSujimura, A.; Yasojima, K.; Hashimoto-Gotch, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997
A>Title: Cloning of Xencops presentinlin-alpha and -beta cDNAs and their differential exp
A.Reference number: JC5390; NUID:97223465; PMID:9070286
A.Accession: JC5391
A>Status: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-449 <TSU>
A.Cross-references: DDBJ:D84428; NID:G1944355; PIDN:BA119571.1; PID:G1944356
A.Experimental source: brain
C.Comment: This protein plays a role in negative regulation of apoptotic cascades durin
C.Superfamily: presentinlin
F.91-109/Domain: transmembrane #status predicted <TM1>
F.143-163/Domain: transmembrane #status predicted <TM2>
F.173-193/Domain: transmembrane #status predicted <TM3>
F.204-221/Domain: transmembrane #status predicted <TM4>
F.230-246/Domain: transmembrane #status predicted <TM5>
F.252-279/Domain: transmembrane #status predicted <TM6>
F.393-410/Domain: transmembrane #status predicted <TM7>

Query Match	61.2%;	Score 1462.5;	DB 2;	Length 449;
Best Local Similarity	64.1%;	Pred. No. 2.8e-106;		
Matches 302;	Conservative 47;	Mismatches 75;	Indels 47;	Gaps 7;

```

QY 2 TELPAPLSTFONAKMSDHTLHNTVRSONDRREQOEHNDRSLGHPPLNNGPOG --- 57
Db 21 SESBPJPSTOVQGVQASGEGLETYS -----HREQNPSTQNN-----BDVPNGRTSGDAY 69
QY 58 NSNQVYEQDEBDEBELLTKGAKHTIMFVYVTCMVVYATIKSVSEFYRKGOLLYTP 117
Db 70 NSSETV---ENSEBELTKRKGARHVTIMFVETLCOMVYATIKSVSEFYRKGOLLYTP 126
QY 118 FTEDTETVQGRALSHSLNNAIMI SVIYVMVTLVLVLYKRCYVHAMLITSLLLFF 177
Db 127 FSEDTSVSGRRLNSTLNTLIMISVILMTFTFLVLYLYKRCYKIHOMLITSLMLFFM 186
QY 178 SFYLGSEFETVYAVDYITVALLIMNFGVGMISIHKGELRFOQAYLIMISALMAVF 237
Db 187 TYLYLSEVFETNIANDYPTLFMVIWNGAVGMICIMHKGPLQOQAYLIMISALMAVF 246
QY 238 IKTLPEMTAMLIAYISYVDLYAVTCLKGPRLMVEPQENETLPALLYSSMMWLVN 257
Db 247 IKTLPEMSAWVILGALSYVDLYAVTCLPQGPRLMVEPQENETLPALLYSSMMWTVG 306
QY 298 MAEGDEAQRVRSKSKKNAESTEREESODTYAENDDGQFSEWEAQRDSHLGPHRSTPES 357

```

Db 307 MAD-SATADGRMNQOVCHIDNTEGANSTV-----ED 338
 QY 358 RAAVOELSSSIAGDDP-EERGVKLAGDFFYSVLVGGKASATASGDMNTTACFAVAILI 416
 Db 339 AAEIRICQUSLSEBDEPERGVKLAGDFFYSVLVGGKAAATASGDMNTTACFAVAILI 398
 QY 417 GLCITLLALLAFKALPALPISITFGLVFPATDYLVQPMQDLAFHOYI 467
 Db 399 GLCITLLALLAFKALPALPISITFGLVFPATDYLVQPMQDLAFHOYI 449

RESULT 9

presentin 2 - human
 M:Alternate names: Alzheimer's disease protein 4
 C:Species: Homo sapiens (man)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Nov-2000
 C/Accession: A56993; 158098
 R:Levy-Jahn, E.; Masco, W.; Poorkaj, P.; Romano, D.M.; Oshima, J.; Pettingell, W.H.; Yu
 Science 269, 973-977, 1995
 A>Title: Candidate gene for the chromosome 1 familial Alzheimer's disease locus.
 A:Reference number: A56993; PMID:95365816; PMID:7638622
 A:Accession: A56993
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-448 <RES>
 A:Cross-references: GB:L43964; NID:G951202; PIDN:AAB59557.1; PID:G951203
 R:Rogaev, E.I.; Sherrington, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; Chi,
 ; Cohen, D.; Lannfelt, L.; Fraser, P.E.; Rommens, J.M.; St George-Hyslop, P.H.
 Nature 376, 773-778, 1995
 A>Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene on C
 A:Reference number: 158098; MUID:95379971; PMID:7651536
 A:Accession: 158098
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122, 'P', 124-448 <RES>
 A:Cross-references: GB:L43964; NID:G950347; PIDN:AAC42012.1; PID:G950348
 C:Genetic: GDB:PSBEN2; ADA; STM2; PS2; ES-1
 A:Gene: GDB:PSBEN2; ADA; STM2; PS2; ES-1
 A:Cross-references: GDB:633044; OMIM:600759
 A:Map position: 1q31-1q42
 C:Superfamily: presentin

Query Match 60.4%; Score 1444; DB 2; Length 448;
 Best Local Similarity 65.0%; Pred. No. 7.6e-105; Indels 42; Gaps 8;
 Matches 303; Conservative 40; Mismatches 81; GRPG-----
 QY 3 ELPAPLSYQNAQMSDNHLSNTVRSQNDNRQENHNR-SLGHPEPLSNRPOGNSRQ 61
 Db 24 EPTPRSCQEGRGQPEDEGNTAQRSGENEDGEDPDRYVCSGV-----GRPG----- 74
 QY 62 VVEQDEDEDELTKYGAQVIMLFVPTLCMIVVAVATIKSVRYTRKQGLIYPTFTED 121
 Db 75 -----LEELTLTKYGAQVIMLFVPTLCMIVVAVATIKSVRYTRKQGLIYPTFTED 127
 QY 122 TETVGORALHSILNAAMISVIVMTLLVLYKRCYKVIHAWLIISLLFFESFIY 181
 Db 128 TTSVQGRLLNSVLTLMISIVVMTIFIVLVLYKRCYKVIHAWLIISLLFFESFIY 187
 QY 182 LGSEVKTNNVAVDYITVALLIWNFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 241
 Db 188 LGSEVKTNNVAVDYITVALLIWNFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 247
 QY 242 PENTAMILLIAVSYVDVAVCLKGPLMLVETAQENETLFPALISSTWMLVMAAG 301
 Db 248 PEMASAVILGALSYVDVAVCLKGPLMLVETAQENETLFPALISSTWMLVMAAG 307
 QY 302 DPBAQRVSKSKNAESTERESQDTVAENDGCFSEMEARQDSHLGPHRSTPESRAV 361
 Db 308 DPSSQAGAL--CLPYDPE-MEEDSYDSFGE--PSYPPVFPPLPLGPG----- 349
 QY 362 QELSSSIAGDEPERGVKLAGDFFYSVLVGGKASATASGDMNTTACFAVAILIGLCIT 421
 Db 362 QELSSSIAGDEPERGVKLAGDFFYSVLVGGKASATASGDMNTTACFAVAILIGLCIT 421

Db 350 EEL-----EEBERGVKLAGDFFYSVLVGGKAAATASGDMNTTACFAVAILIGLCIT 402
 QY 422 LLLLAIFKALPALPISITFGLVFPATDYLVQPMQDLAFHOYI 467
 Db 403 LLLLAIFKALPALPISITFGLVFPATDYLVQPMQDLAFHOYI 448

RESULT 10

seven trans-membrane domain protein AD3LP/ADS - human
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Sep-1999
 C/Accession: I39174
 R:Li, J.; Ma, J.; Potter, H.
 Proc. Natl. Acad. Sci. U.S.A. 92, 12180-12184, 1995
 A>Title: Identification and expression analysis of a potential familial Alzheimer's dis
 A:Reference number: I39174; MUID:96109229; PMID:8618867
 A:Accession: I39174
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-442 <RES>
 A:Cross-references: EMBL:U34349; NID:G1079575; PIDN:AAC50290.1; PID:G1079576
 C:Superfamily: presentin

Query Match 57.6%; Score 1376.5; DB 2; Length 442;
 Best Local Similarity 63.7%; Pred. No. 1.4e-99;
 Matches 286; Conservative 40; Mismatches 82; Indels 41; Gaps 6;

QY 3 ELPAPLSYQNAQMSDNHLSNTVRSQNDNRQENHNR-SLGHPEPLSNRPOGNSRQ 61
 Db 24 EPTPRSCQEGRGQPEDEGNTAQRSGENEDGEDPDRYVCSGV-----GRPG----- 74
 QY 62 VVEQDEDEDELTKYGAQVIMLFVPTLCMIVVAVATIKSVRYTRKQGLIYPTFTED 121
 Db 75 -----LEELTLTKYGAQVIMLFVPTLCMIVVAVATIKSVRYTRKQGLIYPTFTED 127
 QY 122 TETVGORALHSILNAAMISVIVMTLLVLYKRCYKVIHAWLIISLLFFESFIY 181
 Db 128 TTSVQGRLLNSVLTLMISIVVMTIFIVLVLYKRCYKVIHAWLIISLLFFESFIY 187
 QY 182 LGSEVKTNNVAVDYITVALLIWNFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 241
 Db 188 LGSEVKTNNVAVDYITVALLIWNFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 247
 QY 242 PENTAMILLIAVSYVDVAVCLKGPLMLVETAQENETLFPALISSTWMLVMAAG 301
 Db 248 PEMASAVILGALSYVDVAVCLKGPLMLVETAQENETLFPALISSTWMLVMAAG 307
 QY 302 DPBAQRVSKSKNAESTERESQDTVAENDGCFSEMEARQDSHLGPHRSTPESRAV 361
 Db 308 DPSSQAGAL-----PYDPEMEDSYDSFGEPSYPPVFPPLPLGPG----- 348
 QY 362 QELSSSIAGDEPERGVKLAGDFFYSVLVGGKASATASGDMNTTACFAVAILIGLCIT 421
 Db 349 EELER-----EEESQAGVCLGDPFIFYSVLVGGKAAATASGDMNTTACFAVAILIGLCIT 403
 QY 422 LLLLAIFKALPALPISITFGLVFPATDYLVQPMQDLAFHOYI 467
 Db 404 LLLLAIFKALPALPISITFGLVFPATDYLVQPMQDLAFHOYI 448

RESULT 11

protein F55H12.3 (imported) - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
 C/Accession: E89453
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and ww.sanger.ac.uk/Projects/C. ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: E899453
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-836 <STO>
 A:Cross-references: GB:chr_X, PIDs:AAA83176.1; PID:91109863; GSPDB:GN00028; CESP:F35H12
 A:Note: similar to M. musculus S182 protein (GB:U42177)
 C:Genetics:
 A:Gene: F35H12.3
 A:Map position: X

Query Match 44.1%; Score 1054.5; DB 2; Length 836;
 Best Local Similarity 50.9%; Pred. No. 3,6e-74;
 Matches 216; Conservative 70; Mismatches 95; Indels 43; Gaps 6;

QY 64 BODEEDELTLTKYAKAKHYIMLFVPTLCMVVVVAATIKVSFPTKDGQ-LIYPTEDT 122
 Db QDENNVBEAEAKYGHSHYIHLFVPSLCLMALVETWNTITTYSQNGRHLLYTPVRET 91
 QY 123 ETVGQRALHSILNAAIMISVIWMTILLVLYKCYKVYIHAMLISSLLFFPSFTYL 182
 Db DSIYKGLMSLGNALVMLCVVLMITVLLIFPKYKFKYKLIHGMLIVSSFLLEFTTIYV 151
 QY 163 GEVFETVYAVDYIIVALLIMEGVGMISIMKQPLQOAYLIMISALMAVITKPL 242
 Db QEVLSPDVSFALLVTLFGLGNVGVLMGMKCHMKQPLKQCFYLLTMSHLMALVETKLP 211
 QY 243 EWTAMLLIAVISYVDLVAVLCLKGFLRMVLVETAOENRNETLFPALYYSSMTWV--LYNMA 299
 Db EMTVAFVLFVISWMDLVANLTPKGFLRYLVEIQAQRNEIPFALYYSGVIYVLYAV 271
 QY 300 EGDPAQRRVSKNS-----KNAESTERESODTYAENDDGFS 337
 Db ENTTPREPTSSDSNTSTAPEBASCSSETPRPVKYKRIPOKVQIESNTTASTONSGVR 331
 QY 338 EEMEAQRDSHLCPHSTPESRAVOELSSSILAGEDPEERGVKLGDPFIIFYVLGKAS 397
 Db 332 VE-----KEIAERPTVDAN---PHRHEERGVKLGDPFIIFYVLGKAS 376
 QY 398 ATASGDMNTTACFVAALIGLCTLLLLAIFKALPALPISITFGLVFFAFADYVQPM 457
 Db 377 SYF--DWNNTIACYVAALLIGLCTTIVLAVFKRALPALPISIFSGLIFFYCTRWITTPV 434
 QY 458 DGLA 461
 Db 435 TVVS 438

RESULT 12
 S60253
 sel-12 protein - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Sep-1998
 C:Accession: S60253
 R:Levitani, D.; Greenwald, I.
 Nature 377, 351-354, 1995
 A:Title: Facilitation of lin-12-mediated signalling by sel-12, a *Caenorhabditis elegans*
 A:Reference number: S60253; PMID:96032531; PMID:756691
 A:Accession: S60253
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-461 <LEV>
 A:Cross-references: EMBL:U35660
 C:Superfamily: preeinflin

Query Match 40.3%; Score 963.5; DB 2; Length 461;
 Best Local Similarity 49.5%; Pred. No. 2,2e-67;
 Matches 203; Conservative 64; Mismatches 100; Indels 43; Gaps 6;

QY 64 BODEEDELTLTKYAKHYIMLFVPTLCMVVVVAATIKVSFPTKDGQ-LIYPTEDT 122
 Db QEDENVBEAEAKYGHSHYIHLFVPSLCLMALVETWNTITTYSQNGRHLLSHPVRRT 91
 QY 123 ETVGQRALHSILNAAIMISVIWMTILLVLYKCYKVYIHAMLISSLLFFPSFTYL 182

QY 163 GEVFETVYAVDYIIVALLIMEGVGMISIMKQPLQOAYLIMISALMAVITKPL 242
 Db QEVLSPDVSFALLVTLFGLGNVGVLMGMKCHMKQPLKQCFYLLTMSHLMALVETKLP 211
 QY 243 EWTAMLLIAVISYVDLVAVLCLKGFLRMVLVETAOENRNETLFPALYYSSMTWV--LYNMA 299
 Db EMTVAFVLFVISWMDLVANLTPKGFLRYLVEIQAQRNEIPFALYYSGVIYVLYAV 271
 QY 300 EGDPAQRRVSKNS-----KNAESTERESODTYAENDDGFS 337
 Db ENTTPREPTSSDSNTSTAPEBASCSSETPRPVKYKRIPOKVQIESNTTASTONSGVR 331
 QY 338 EEMEAQRDSHLCPHSTPESRAVOELSSSILAGEDPEERGVKLGDPFIIFYVLGKAS 397
 Db 332 VE-----KEIAERPTVDAN---PHRHEERGVKLGDPFIIFYVLGKAS 376
 QY 398 ATASGDMNTTACFVAALIGLCTLLLLAIFKALPALPISITFGLVFFAFADYVQPM 457
 Db 377 SYF--DWNNTIACYVAALLIGLCTTIVLAVFKRALPALPISIFSGLIFFYCTRWITTPV 434
 QY 458 DGLA 461
 Db 435 TVVS 438

QY 123 ETVGQRALHSILNAAIMISVIWMTILLVLYKCYKVYIHAMLISSLLFFPSFTYL 182

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:50:51 / Search time 17 Seconds
(without alignments)

1430.398 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391
Sequence: 1 MTELPAPLSYFGNAQMSDN.....ATDYLVPPMDQLARHGFYI 467

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	99.5	467	1 PSN1_HUMAN	P49768 homo sapien
2	2354	98.5	467	1 PSN1_MACFA	Q8HW55 macaca fasc
3	2266	94.8	467	1 PSN1_MICMU	P79802 microcebus
4	2228	93.2	467	1 PSN1_MOUSE	P49769 mus musculu
5	2200.5	92.0	468	1 PSN1_RAT	P97887 rattus norv
6	2175.5	91.0	478	1 PSN1_BOVIN	Q9X977 bos taurus
7	1801	75.3	433	1 PSN1_XENLA	O12976 xenopus lae
8	1614.5	67.5	456	1 PSN1_BRAKE	Q9W6C7 brachydanto
9	1462.5	61.2	449	1 PSN2_XENLA	O12977 xenopus lae
10	1452	60.7	448	1 PSN2_HUMAN	P79801 microcebus
11	1440	60.2	445	1 PSN2_MICMU	P79801 microcebus
12	1432.5	59.9	449	1 PSN2_BOVIN	Q9X976 bos taurus
13	1430	59.8	448	1 PSN2_RAT	O88777 rattus norv
14	1428	59.7	448	1 PSN2_MOUSE	O61144 mus musculu
15	1415	59.2	441	1 PSN2_BRAKE	Q90764 brachydanto
16	1174.5	49.1	541	1 PSN1_DROME	O02194 drosophila
17	1054.5	44.1	444	1 PSN1_CAEEL	P52166 caenorhabdi
18	539.5	22.6	453	1 PSN1_ARATH	O64668 arabidopsis
19	538	22.5	397	1 PSN1_ARATH	O64668 arabidopsis
20	505	21.1	358	1 PSN1_CAEEL	O02100 caenorhabdi
21	309.5	12.9	465	1 SPK4_CAEEL	O01608 caenorhabdi
22	120.5	5.0	2386	1 RAD3_SCHPO	O02099 schizosacch
23	117	4.9	601	1 OAR_DROME	P22270 drosophila
24	114.5	4.8	323	1 CD47_HUMAN	Q08722 homo sapien
25	108.5	4.5	971	1 Y277_MYCPN	P75387 mycoplasma
26	107.5	4.5	2365	1 CCAL_MOUSE	O88427 mus musculu
27	107.5	4.5	488	1 YB91_YEAST	P38412 saccharomyc
28	106.5	4.5	436	1 A2AR_CARAU	P32251 carassius a
29	104	4.3	520	1 PS12_HUMAN	O88428 homo sapien
30	103.5	4.3	354	1 C3X1_MOUSE	O92069 mus musculu
31	102	4.3	713	1 ACCE_HUMAN	O18007 caenorhabdi
32	102	4.3	1580	1 ACCE_HUMAN	Q09428 homo sapien
33	101.5	4.2	754	1 YCA1_ECOLI	P37443 escherichia

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	2378	99.5	467	1 PSN1_HUMAN	P49768 homo sapien
2	2354	98.5	467	1 PSN1_MACFA	Q8HW55 macaca fasc
3	2266	94.8	467	1 PSN1_MICMU	P79802 microcebus
4	2228	93.2	467	1 PSN1_MOUSE	P49769 mus musculu
5	2200.5	92.0	468	1 PSN1_RAT	P97887 rattus norv
6	2175.5	91.0	478	1 PSN1_BOVIN	Q9X977 bos taurus
7	1801	75.3	433	1 PSN1_XENLA	O12976 xenopus lae
8	1614.5	67.5	456	1 PSN1_BRAKE	Q9W6C7 brachydanto
9	1462.5	61.2	449	1 PSN2_XENLA	O12977 xenopus lae
10	1452	60.7	448	1 PSN2_HUMAN	P79801 microcebus
11	1440	60.2	445	1 PSN2_MICMU	P79801 microcebus
12	1432.5	59.9	449	1 PSN2_BOVIN	Q9X976 bos taurus
13	1430	59.8	448	1 PSN2_RAT	O88777 rattus norv
14	1428	59.7	448	1 PSN2_MOUSE	O61144 mus musculu
15	1415	59.2	441	1 PSN2_BRAKE	Q90764 brachydanto
16	1174.5	49.1	541	1 PSN1_DROME	O02194 drosophila
17	1054.5	44.1	444	1 PSN1_CAEEL	P52166 caenorhabdi
18	539.5	22.6	453	1 PSN1_ARATH	O64668 arabidopsis
19	538	22.5	397	1 PSN1_ARATH	O64668 arabidopsis
20	505	21.1	358	1 PSN1_CAEEL	O02100 caenorhabdi
21	309.5	12.9	465	1 SPK4_CAEEL	O01608 caenorhabdi
22	120.5	5.0	2386	1 RAD3_SCHPO	O02099 schizosacch
23	117	4.9	601	1 OAR_DROME	P22270 drosophila
24	114.5	4.8	323	1 CD47_HUMAN	Q08722 homo sapien
25	108.5	4.5	971	1 Y277_MYCPN	P75387 mycoplasma
26	107.5	4.5	2365	1 CCAL_MOUSE	O88427 mus musculu
27	107.5	4.5	488	1 YB91_YEAST	P38412 saccharomyc
28	106.5	4.5	436	1 A2AR_CARAU	P32251 carassius a
29	104	4.3	520	1 PS12_HUMAN	O88428 homo sapien
30	103.5	4.3	354	1 C3X1_MOUSE	O92069 mus musculu
31	102	4.3	713	1 ACCE_HUMAN	O18007 caenorhabdi
32	102	4.3	1580	1 ACCE_HUMAN	Q09428 homo sapien
33	101.5	4.2	754	1 YCA1_ECOLI	P37443 escherichia

- RA Pellerier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Crandall C.,
RA Brule T., Vailion O., Friedlander L., Samson G., Broctier P.,
RA Cure S., Segreus B., Aniere P., Samain S., Crespeau H., Abbaei N.,
RA Aitch N., Bocus D., Dickhoff R., Dors M., Dubois I., Friedman C.,
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RA Vachette B., Bellemere C., Belser C., Besnard-Gonnet M.,
RA Batoli-Marel D., Boutard M., Briez-Silla S., Combette S.,
RA Dutoise-Laurent V., Ferron C., Lechaplais C., Louesse C., Muesel D.,
RA Magdeleinat G., Pateau E., Petit E., Straval-Tukhlewicz P., Trybou A.,
RA Vega-Carraz N., Bataille E., Bluet E., Bortolais I., Dubois M.,
RA Dumont C., Gerin T., Haffray S., Hammadi R., Muanga J., Pellouin V.,
RA Robert D., Wunderle E., Gauguier G., Roy A., Sainte-Marthe L.,
RA Verdier J., Verdier-Discale C., Hillier L.M., Fulton L., McPherson J.,
RA Maesda F., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W.,
RA Queller F., Waterston R., Hood L., Weissbach J.,
RA "The DNA sequence and analysis of human chromosome 14.",
RL Nature 421:601-607(2003).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Skin;
RA MEDLINE=2238957; PubMed=12477932;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheer T.E.,
RA Brownstein M.J., Ustin T.B., Toshitsugu S., Carninci P., Prange C.,
RA Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gundacker P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherich A., Schein J.E., Jones S.J.W., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1.113 FROM N.A.
RA Tsujimura A., Hashimoto-Gotoh T.,
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=96160372; PubMed=8574969;
RA Kovacs D.W., Fausett H.J., Page K.J., Kim T.-W., Moir R.D.,
RA Merliam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
RA Felsenstein K.W., Hyman B.T., Tanzi R.E., Masco W.,
RA "Alzheimer-associated presenilin 1 and 2: neuronal expression in
RT brain and localization to intracellular membranes in mammalian
RT cells.",
RL Nat. Med. 2:224-229(1996).
RN [10]
RP PROCESSING
RX MEDLINE=97317150; PubMed=9173929;
RA Podlasky W.B., Citron M., Amaratne P., Sherrington R., Xia W.,
RA Zhang J., Diehl T., Levesque G., Fraser P., Haas C., Koo E.H.,
RA Schubert P., St George-Hyslop P., Teplow D.B., Selkoe D.J.,
RT "Presenilin proteins undergo heterogeneous endoproteolysis between
RT Thr91 and Ala299 and occur as stable N- and C-terminal fragments in
RT normal and Alzheimer brain tissue.",
RL Neurobiol. Dis. 3:325-337(1997).
RN [11]
RP FUNCTION, AND MUTAGENESIS OF MET-292.
RX MEDLINE=20014554; PubMed=10545183;
RA Steiner H., Romig H., Pesold B., Philipp U., Baader M., Citron M.,
RA Loeschner H., Jacobsen H., Haas C.,
RT "Amyloidogenic function of the Alzheimer's disease-associated
RP
- RT Presenilin 1 in the absence of endoproteolysis.",
RL Biochemistry 38:14600-14605(1999).
RN [12]
RP FUNCTION.
RX MEDLINE=20062913; PubMed=10593990;
RA Ray W.J., Yao M., Mumm J., Schroeder E.H., Safirig P., Wolfe M.,
RA Selkoe D.J., Kopan R., Goate A.M.,
RT "Cell surface presenilin-1 participates in the gamma-secretase-like
RT proteolysis of Notch.",
RL J. Biol. Chem. 274:36801-36807(1999).
RN [13]
RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
RX MEDLINE=99221485; PubMed=10206644;
RA Wolfe M.S., Xia W., Ostaszewski B.L., Diehl T.S., Kimberly W.T.,
RA Selkoe D.J.,
RT "Two transmembrane aspartates in presenilin-1 required for presenilin
RT endoproteolysis and gamma-secretase activity.",
RL Nature 398:513-517(1999).
RN [14]
RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
RX MEDLINE=20359495; PubMed=10899933;
RA Berzovska O., Jack C., McLean P., Aster J.C., Hicks C., Xia W.,
RA Wolfe M.S., Kimberly W.T., Weinmaster G., Selkoe D.J., Hyman B.T.,
RT "Aspartate mutations in presenilin and gamma-secretase inhibitors both
RT impair notch proteolysis and nuclear translocation with relative
RT preservation of notch signaling.",
RL J. Neurochem. 75:583-593(2000).
RN [15]
RP FUNCTION, AND MUTAGENESIS OF LEU-286.
RX MEDLINE=20283925; PubMed=10811883;
RA Kulic L., Walter J., Multhaup G., Teplow D.B., Baumeister R.,
RA Romig H., Capell A., Steiner H., Haas C.,
RT "Separation of presenilin function in amyloid beta-peptide generation
RT and endoproteolysis of Notch.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:5913-5918(2000).
RN [16]
RP FUNCTION.
RX PubMed=1126248;
RA Bakli L., Marandaud P., Efthimiopoulos S., Georgakopoulos A., Wen P.,
RA Cui W., Shioi U., Koo E., Oawa M., Friedrich V.L., Robakis N.K.,
RT "Presenilin-1 binds cytoplasmic epithelial cadherin, inhibits
RT cadherin/p120 association, and regulates stability and function of
RT the cadherin/catenin adhesion complex.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:2381-2386(2001).
RN [17]
RP INTERACTIONS WITH FHLA AND FHLB.
RX MEDLINE=98099802; PubMed=9437013;
RA Zhang W., Han S.W., McKee D.W., Goate A., Wu J.Y.,
RT "Interaction of presenilin with the filament family of actin-binding
RT proteins.",
RL J. Neurosci. 18:914-922(1998).
RN [18]
RP INTERACTION WITH DELTA-2 CATELIN.
RX MEDLINE=99155075; PubMed=10037471;
RA Levesque G., Yu G., Nishimura M., Zhang D.M., Levesque L., Yu H.,
RA Xu D., Liang Y., Kogaeva E., Ikeda W., Dutche M., Murgolo N., Wang L.,
RA Vanderveere P., Bayne M.L., Strader C.D., Rommens J.M., Fraser P.B.,
RA St George-Hyslop P.,
RT "Presenilin interact with armadillo proteins including
RT neural-specific plakophilin-related protein and beta-catenin.",
RL J. Neurochem. 72:999-1008(1999).
RN [19]
RP INTERACTION WITH HERPUD1.
RX MEDLINE=2193537; PubMed=11799129;
RA Sai X., Kawamura Y., Kokame K., Yamaguchi H., Shiraiishi H., Suzuki R.,
RA Suzuki T., Kawachi M., Miyata T., Kitamura T., De Strooper B.,
RA Yanagisawa K., Komano H.,
RT "endoplasmic reticulum stress-inducible protein, Herp, enhances
RT presenilin-mediated generation of amyloid beta-protein.",
RL J. Biol. Chem. 277:12915-12920(2002).
RN [20]
RP COMPONENT OF A GAMMA-SECRETASE COMPLEX WITH PEN2, PSEN1/PSEN2 AND
RP NCSTN.

DB	421	TLLBLAI	PKKAL	PLPISIT	GLVFPAT	DTLVOP	FMQCL	LFHO	YI	467
cy	421	TLLBLAI	PKKAL	PLPISIT	GLVFPAT	DTLVOP	FMQCL	LFHO	YI	467
Db	421	TLLBLAI	PKKAL	PLPISIT	GLVFPAT	DTLVOP	FMQCL	LFHO	YI	467
RESULT 3										
PSN1	MICMU									
ID	PSN1	MICMU								
AC	P79802									
DT	15-JUL-1999									
DT	15-JUL-1999									
DT	15-JUL-1999									
DT	15-MAR-2004									
DE	Presentin 1 (PS-1)									
OS	PSEN1 OR PSN1 OR PSI									
OC	Microcebus murinus (Lesser mouse lemur)									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Strepsirrhini; Chirogaleidae;									
OC	Microcebus									
OC	NCBI_TaxID=30608;									
OC	[1]									
OC	SEQUENCE FROM N.A. (ISCFORMS I-463 AND I-467).									
OC	TISSUE=Brain;									
OC	MEDLINE=9707199; PubMed=8920931;									
OC	Calenda A., Nestre-Frances N., Czech C., Pradier L., Bone N.,									
OC	Bellis M.;									
OC	"Molecular cloning, sequencing, and brain expression of the									
OC	Presentin 1 gene in Microcebus murinus."									
OC	Biochem. Biophys. Res. Commun. 228:430-439 (1996).									
OC	-I- FUNCTION: Probable catalytic subunit of the gamma-secretase									
OC	complex, an endoprotease complex that catalyzes the intramembrane									
OC	cleavage of integral membrane proteins such as Notch receptors and									
OC	APP (beta-amyloid precursor protein). Requires the other members									
OC	of the gamma-secretase complex to have a protease activity. May									
OC	play a role in intracellular signaling and gene expression or in									
OC	linking chromatin to the nuclear membrane. Regulates epithelial-									
OC	cadherin function (By similarity).									
OC	-I- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a									
OC	complex composed of a presentin homodimer (PSN1 or PSN2),									
OC	nicastrin (NCTN), APH1 (APH1A or APH1B) and PEN2. Such minimal									
OC	complex is sufficient for secretase activity, although other									
OC	components may exist. Predominantly heterodimer of a N-terminal									
OC	(NTP) and a C-terminal (CTP) endoproteolytic fragment.									
OC	Associates with proteolytic processed C-terminal fragments C83 and									
OC	C99 of the amyloid precursor protein (APP). Associates with									
OC	NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and									
OC	plakophilin 4. Interacts with DOK3. Interacts with HERPUD1, FLNA									
OC	and PLNB (By similarity).									
OC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and									
OC	endoplasmic reticulum (By similarity).									
OC	-I- ALTERNATIVE PRODUCTS:									
OC	Event=Alternative Splicing; Named isoforms=2;									
OC	Name=I-467;									
OC	IsoId=P79802-1; Sequence=Displayed;									
OC	Name=I-463;									
OC	IsoId=P79802-2; Sequence=VSP 005193;									
OC	-I- TISSUE SPECIFICITY: Found predominantly in neurons of the									
OC	different cortical layers and hippocampus but also in subcortical									
OC	structures.									
OC	-I- PTM: Phosphorylated on serine residues (By similarity).									
OC	-I- SIMILARITY: Belongs to the presentin family.									
OC	-----									
OC	This SWISS-PROT entry is copyright. It is produced through a collaboration									
OC	between the Swiss Institute of Bioinformatics and the E									

[illegible]

QY 300 EGDPEAQRYSKSNKNAE-----STERESODTYAENDGSESEMEAPORSHUG 349
 DB 301 EGDPEAQRYSKSNKNAE-----STERESODTYAENDGSESEMEAPORSHUG 360
 QY 350 PHSSTPESRAVOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTIA 409
 DB 361 PHSSTPESRAVOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTIA 420
 QY 410 CPVALILGLCTLLLLAIFKKALPALPISITTEGLVVFADPDYVOPFMOCLAFHOPIYI 467
 DB 421 CPVALILGLCTLLLLAIFKKALPALPISITTEGLVVFADPDYVOPFMOCLAFHOPIYI 478

RESULT 7
 PSN1_XENLA STANDARD; PRT; 433 AA.
 ID PSN1_XENLA STANDARD; PRT; 433 AA.
 AC 012976;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Presentin alpha.
 GN PS-ALPHA.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCB1_Taxid=8355;
 RX MEDLINE=97223465; PubMed=9070286;
 RA Tsuchiya A., Yasojima K., Hashimoto-Gotoh T.;
 RT "Cloning of Xenopus presentin-alpha and -beta cDNAs and their
 differential expression in oogenesis and embryogenesis.";
 RL Biochem. Biophys. Res. Commun. 231:392-396(1997).
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors (By
 similarity). May play a role in negative regulation of apoptotic
 cascades during oogenesis and embryogenesis, and in
 developmentally matured tissues such as brain tissue.
 CC -1- SUBUNIT: Homodimer. Probable component of the gamma-secretase
 complex, a complex composed of a presentin homodimer (PS-alpha or
 PS-beta), nicastrin (NCTN), Aph1 and PEN2 (probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highest expression in ovaries and to a lesser
 extent in testis, intestine, kidney, brain, eye and lung. Weak
 expression in liver and heart. Present in trace amounts in
 skeletal muscle.
 CC -1- DEVELOPMENTAL STAGE: Abundant in early stages of oogenesis. The
 expression is rapidly reduced between meiotic maturation and
 fertilization stages.
 CC -1- SIMILARITY: Belongs to the presentin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

DR EMBL; D84427; BAA19570.1; -
 DR PIR; JCS390; JCS390.
 DR MEROPS; A22.001; -
 DR InterPro; IPR006639; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presentin_1.
 DR PRINTS; PR01072; PRESENTIN.
 DR SMART; SM00730; PSN.1.
 KW Transmembrane; Glycoprotein.
 FT TRANSMEM 48 68
 FT TRANSMEM 99 119
 FT POTENTIAL.
 FT POTENTIAL.

FT TRANSMEM 127 147
 FT TRANSMEM 161 181
 FT TRANSMEM 184 204
 FT TRANSMEM 210 230
 FT TRANSMEM 247 267
 FT TRANSMEM 374 394
 FT TRANSMEM 399 419
 FT TRANSMEM 445 465
 FT CAROXYD 371 391
 FT CAROXYD 371 391
 SQ SEQUENCE 433 AA; 48301 MW; 71CCEB3FEB93C0AF CRC64;

Query Match 75.3%; Score 1801; DB 1; Length 433;
 Best Local Similarity 82.8%; Pred. No. 3.8e-118;
 Matches 355; Conservative 26; Mismatches 48; Indels 0; Gaps 0;

QY 39 NDRSLGPEPLSGRPGNGRQVVEODEDEELTKYGAHYIMFVPTLCMVVVA 98
 DB 5 SERNSNSESQSNQGTSSQVLEODEDEDEELTKYGAHYIMFVPTLCMVVVA 64
 QY 99 TIKSVSFYTRKDGOLITPTEDTEVQGRALSHILNAIMTSIVVMTLLVLYKRC 158
 DB 65 TIKSVSFYTRPDGOLITPTEDTESVQGRALSHILNAIMTSIVVMTLLVLYKRC 124
 QY 159 YKVIHAWLIIISLLPFESFYLGVEKTVNAVDTYVALLIMFGVGMISIMKGP 218
 DB 125 YKVIHAWLIIISLLPFESFYLGVEKTVNAVDTYVALLIMFGVGMISIMKGP 184
 QY 219 LRLQAVLIMISALMAVFIKLPMTAMLLAVISYVDLVAVLCGLPLMVEYTAQR 278
 DB 185 LRLQAVLIMISALMAVFIKLPMTAMLLAVISYVDLVAVLCGLPLMVEYTAQR 244
 QY 279 NETLPAIYSTWVIMVNAEGDEAQRYSKSNKNAESTERESODTYAENDGCGFSE 338
 DB 245 NETLPAIYSTWVIMVNAEGDEAQRYSKSNKNAESTERESODTYAENDGCGFSE 304
 QY 339 EWEACRSHLGHPRSTPESRAVOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASA 398
 DB 305 EWEACRSHLGHPRSTPESRAVOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASA 364
 QY 399 TASGDMNTTIAFPVALILGLCTLLLLAIFKKALPALPISITTEGLVVFADPDYVOPFMD 458
 DB 365 TASGDMNTTIAFPVALILGLCTLLLLAIFKKALPALPISITTEGLVVFADPDYVOPFMD 424
 QY 459 QLAHQFYI 467
 DB 425 QLAHQFYI 433

RESULT 8
 PSN1_BRARE STANDARD; PRT; 456 AA.
 ID PSN1_BRARE STANDARD; PRT; 456 AA.
 AC 096677;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Presentin 1 (PS1) (ZF-PS1).
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_Taxid=7955;
 RX MEDLINE=9452701; PubMed=10521267;
 RA Leimer U., Lun K., Romig H., Walter J., Gruenberg J., Brand M.,
 Haase C.;
 RT "Zebrafish (Danio rerio) presentin promotes aberrant amyloid
 beta-peptide production and requires a critical aspartate residue for
 its function in amyloidogenesis.";
 RL Biochemistry 38:13602-13609(1999).
 [2]
 SEQUENCE FROM N.A.

CC TISSUE-Embryo;
 CC Strassberg R.U.;
 CC Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors (By
 CC similarity).
 CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
 CC complex composed of a presenilin homodimer (PSEN1 or PSEN2),
 CC nicastrin, APL1 and PEN2 (probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 CC endoplasmic reticulum (By similarity).
 CC -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
 CC Ubiquitously expressed during embryogenesis.
 CC -1- PTM: Cleaved, probably due to some autocleavage.
 CC -1- SIMILARITY: Belongs to the presenilin family.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, AJ132931; CAB40386.1; -
 CC EMBL, BC054639; AAH54639.1; ALT_INIT.
 CC MEROPS: A22.001; -
 CC DR ZFIN, ZDB-GENE-991119-4; pscn1.
 CC DR InterPro, IPR006639; Peptidase_A22.
 CC DR InterPro, IPR001108; Peptidase_A22A.
 CC DR Pfam, PF01080; Presenilin; 1.
 CC DR PRINTS, PRO1072; PRESENILIN.
 CC DR SMART, SM00730; PSN; 1.
 CC KM Transmembrane; Endoplasmic reticulum; Golgi stack.
 CC FT TRANSMEM 71 91 POTENTIAL.
 CC FT TRANSMEM 122 142 POTENTIAL.
 CC FT TRANSMEM 155 175 POTENTIAL.
 CC FT TRANSMEM 184 204 POTENTIAL.
 CC FT TRANSMEM 210 230 POTENTIAL.
 CC FT TRANSMEM 233 253 POTENTIAL.
 CC FT TRANSMEM 337 417 POTENTIAL.
 CC FT TRANSMEM 422 442 POTENTIAL.
 CC FT MOTIFGEN 374 374 D->A: ABOLOSSES ITS ENDOPROTEOLYSIS.
 CC FT CONFLICT 308 308 PROBABLY LOSS OF FUNCTION.
 CC FT CONFLICT 317 317 MISSING (IN REF. 2).
 CC FT CONFLICT 317 317 A -> P (IN REF. 2).
 CC SQ SEQUENCE 456 AA; 50981 MW; B90C42280C874F8D CRC64;

Query Match 67.5%; Score 1614.5; DB 1; Length 456;
 Best Local Similarity 72.1%; Pred. No. 3.8e-105;
 Matches 334; Conservative 32; Mismatches 78; Indels 19; Gaps 7;

QY 12 QNAQMSSEDNHLSNTRVRSQNDNEROEHNDRSLGHEPELSNGRPOGNSQVY-EQDEBED 70
 Db 6 QNAANNVNDGMDTRHRSSTAPSRNVEVLNGP-----PTAPPPQVVTDSBED 58
 QY 71 EELITKYGAKHYIMFVPTLCMVVAVATIKSVSYTKGQ-QILYTFETDTEVGORA 129
 Db 59 EELITKYGAKHYIMFVPTLCMVVAVATIKSVSYTKGQ-QILYTFETDTEVGORA 118
 QY 130 LHSILNAAIMISVIVMTLLVLLVLYKRCYKIHAMLIISSLLILFFPSFYLYGEVEFTY 189
 Db 119 LHSMLNAILMISVIVMTLLVLLVLYKRCYKIQMWLFPSNLLILFFSLIYLGVEFTY 178
 QY 130 NNAVDYIYVALLINFGVVGMSIHWKGPLRLOQNYLMISALVALVITKLPETANLI 249
 Db 179 NNAVDYIYVALLINFGVVGMSIHWKGPLRLOQNYLMISALVALVITKLPETANLI 238
 QY 250 LAVISVYDIAVAVLCKGRLMLVETAOENETLFPALIVYSTWVWLVNNAAGDEAQRV 309
 Db 239 LAIVSVYDIAVAVLCKGRLMLVETAOENETLFPALIVYSTWVWLVNNAAGDEAQRV 294

QY 310 SKNSKNAESTERE---SODTYAENDDGFSEHWEKQSDSHLCPHRSPTESRAVQELSS 366
 Db 295 -NNSSHVPQOEKQVAVAPTAQEDDGFTPMVVHQQHQPKWSTESRRQIDEMPS 353
 QY 367 S--ILGDEPEERGVKLGDFIFYSVLVQKASATASGMNTTIAFCVAILIGLCTLL 424
 Db 354 ARPPPADDEERGVKLGDFIFYSVLVQKASATASGMNTTIAFCVAILIGLCTLL 413
 QY 425 LAIFKALPALPISITFGVVFATDYLYQPFMDQAFHQFYI 467
 Db 414 LAIFKALPALPISITFGVVFATDYLYQPFMDQAFHQFYI 456
 RESULT 9
 PSN2_XENLA
 ID PSN2_XENLA STANDARD; PRT; 449 AA.
 AC 012977;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Presenilin beta.
 GN PS-BETA.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97223465; PubMed=9070286;
 RA Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;
 RT "Cloning of Xenopus presenilin-alpha and -beta cDNAs and their
 RT differential expression in oogenesis and embryogenesis.";
 RT Biochem. Biophys. Res. Commun. 231:392-396 (1997).
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors (By
 CC similarity). May play a role in negative regulation of apoptotic
 CC cascades during oogenesis and embryogenesis, and in
 CC developmentally matured tissues such as brain tissue.
 CC -1- SUBUNIT: Homodimer. Probable component of the gamma-secretase
 CC complex, a complex composed of a presenilin homodimer (PS-alpha or
 CC PS-beta), nicastrin (NCTN), APL1 and PEN2 (probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highest expression in ovaries and to a lesser
 CC extent in kidney, brain, eye and lung. Weak expression in testis,
 CC intestine, liver and heart. Present in trace amounts in skeletal
 CC muscle.
 CC -1- DEVELOPMENTAL STAGE: Abundant in early stages of oogenesis after
 CC which it is nearly constant.
 CC -1- SIMILARITY: Belongs to the presenilin family.
 CC -----
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 CC -----
 CC EMBL, D84428; BAA19571.1; -
 CC PIR, JCS391; JCS391.
 CC DR MEROPS: A22.002; -
 CC DR InterPro, IPR006639; Peptidase_A22.
 CC DR InterPro, IPR001108; Peptidase_A22A.
 CC Pfam, PF01080; Presenilin; 1.
 CC PRINTS, PRO1072; PRESENILIN.
 CC SMART, SM00730; PSN; 1.
 CC KM Transmembrane; Glycoprotein.
 CC FT TRANSMEM 92 112 POTENTIAL.
 CC FT TRANSMEM 142 162 POTENTIAL.
 CC FT TRANSMEM 170 190 POTENTIAL.

RL J. Neurosci. 18:914-922(1998).
 RN [10]
 RP MUTAGENESIS OF ASP-366.
 RP MEDLINE=99428546; PubMed=10497236;
 RA Steiner H., Dufk K., Capell A., Romig H., Grim M.G., Lincoln S.,
 RA Hardy J., Yu X., Picciano M., Fichteler K., Clifton M., Kogan R.,
 RA Persold B., Beck S., Baader M., Tomlita T., Iwatsubo T., Baumeister R.,
 RA Haas C.;
 RA "A loss of function mutation of presenilin-2 interferes with amyloid
 RT beta-peptide production and notch signaling.";
 RL J. Biol. Chem. 274:28669-28673(1999).
 RN [11]
 RP MUTAGENESIS OF ASP-263 AND ASP-366.
 RP MEDLINE=20119269; PubMed=10652302;
 RA Kimberly W.T., Xia W., Rahmati T., Wolfe M.S., Selkoe D.J.;
 RT "The transmembrane aspartates in presenilin 1 and 2 are obligatory for
 RL gamma-secretase activity and amyloid beta-protein generation.";
 RL J. Biol. Chem. 275:3173-3178(2000).
 RN [12]
 RP INTERACTION WITH HERPDL.
 RP MEDLINE=21935327; PubMed=11799129;
 RA Sai K., Kawamura Y., Koxame K., Yamaguchi H., Shiraishi H., Suzuki R.,
 RA Suzuki T., Kawachi M., Miyata K., Kitamura T., De Strooper B.,
 RA Yanagisawa K., Komano H.;
 RA "Endoplasmic reticulum stress-inducible protein, Herp, enhances
 RT presenilin-mediated generation of amyloid beta-protein.";
 RL J. Biol. Chem. 277:12915-12920(2002).
 RN [13]
 RP REVIEW ON VARIANTS.
 RP MEDLINE=96180715; PubMed=9521418;
 RA Cruts M., van Broeckhoven C.;
 RA "Presenilin mutations in Alzheimer's disease.";
 RL Hum. Mutat. 11:183-190(1998).
 RN [14]
 RP VARIANT AD HIS-62.
 RP MEDLINE=998046005; PubMed=93984602;
 RA Cruts M., van Duyn C.M., Backhovens H., van den Broeck M.,
 RA Wehrter A., Sernaele S., Sherrington R., Hutton M., Hardy J.,
 RA St George-Hyslop P.H., Hoffman A., van Broeckhoven C.;
 RT "Estimation of the genetic contribution of presenilin-1 and -2
 RT mutations in a population-based study of presenile Alzheimer
 RT disease.";
 RL Hum. Mol. Genet. 7:43-51(1998).
 RN [15]
 RP VARIANT AD ILE-148.
 RP Lao J.I., Beyer K., Fernandez-Novoa L., Cacabelos R.;
 RA "A novel mutation in the predicted TM2 domain of the presenilin 2 gene
 RT in Spanish patient with late-onset Alzheimer's disease.";
 RL Neurogenetics 1:293-296(1998).
 RN [16]
 RP VARIANTS AD PRO-122 AND ILE-239.
 RP MEDLINE=20100613; PubMed=10651141;
 RA Pincku U., Meller-Thomsen T., Mann U., Eggers C., Makseleiner J.,
 RA Meins W., Binetti G., Alberici A., Hock C., Nitsch R.M., Gal A.;
 RA "High prevalence of pathogenic mutations in patients with early-onset
 RT dementia detected by sequence analyses of four different genes.";
 RL Am. J. Hum. Genet. 66:110-117(2000).
 RN -1-
 RP FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors and
 CC APP (beta-amyloid precursor protein). Regulates the other members
 CC of the gamma-secretase complex to have a protease activity. May
 CC play a role in intracellular signaling and gene expression or in
 CC linking chromatin to the nuclear membrane. May function in the
 CC cytoplasmic partitioning of proteins.
 CC -1-
 CC SUBUNIT: Interacts with DOK3 (By similarity). Homodimer.
 CC Component of the gamma-secretase complex, a complex composed of a
 CC presenilin homodimer (PSEN1 or PSEN2), nicastrin (NCSTN), APL1
 CC (APH1A or APL1B) and PEN2. Such minimal complex is sufficient for
 CC secretase activity although other components may exist. Interacts
 CC with HERPDL, FUNA and FLNB.
 CC -1-
 CC SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 CC endoplasmic reticulum.

```

CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC
CC Name=1;
CC IsoId=P49810-1; Sequence=displayed;
CC Name=2;
CC IsoId=P49810-2; Sequence=VSP_005194;
CC -1- TRISUS SPECIFICITY. Isoform 1 is seen in the placenta, skeletal
CC muscle and heart while isoform 2 is seen in the heart, brain,
CC placenta, liver, skeletal muscle and kidney.
CC -1- PM: Heterogeneous proteolytic processing generates N-terminal and
CC C-terminal fragments.
CC -1- PM: Phosphorylated on serine residues.
CC -1- DISEASE: Defects in PSEN2 are a cause of early-onset Alzheimer
CC disease (AD) [MIM:104300], which is the most severe form of the
CC disease, with complete penetrance and an onset occurring as early
CC as 30 years of age. The second form is late-onset AD (LOAD), with
CC mean age of onset greater than 58 years. AD is an autosomal
CC dominant neurodegenerative disorder characterized by progressive
CC dementia, parkinsonism, and deposition of fibrillar amyloid
CC proteins as intraneuronal neurofibrillary tangles, extracellular
CC amyloid plaques and vascular amyloid deposits.
CC -1- DISEASE: Three causative genes have been identified that when
CC mutated lead to presenile Alzheimer's disease: APP (amyloid
CC precursor protein gene), PSEN1 and PSEN2. These three genes
CC account for half of the families with autosomal dominant presenile
CC AD, which represent approximately 10% of the whole AD population.
CC In addition, apolipoprotein E has been identified as a risk-
CC modifying locus.
CC -1- SIMILARITY: Belongs to the presenilin family.
CC -1- DATABASE: NAME=Alzheimer Research Forum;

```

Query Match	60.7%	Score 1452	DB 1	Length 448
Best Local Similarity	65.2%	Pred. No. 7,4e-94		
Matches 304	Conservative 40	Mismatches 80	Indels 42	Gaps 8
QY	3	ELPAPLSYFQNAQMSQEDNHSNTVRSQNDNRERQEHNDNR-SLGHPEPLSGRPOGNSRQ	61	
DB	24	ESPFRSQEQRQPEDEGENTAMQRSQENEDGEDDEDPRTYQSGYP-----GRPG----	74	
QY	62	VVEQDEEDELTLKYGAKHYIMLFVPTLCMVVVADTKASFPTRQGLITPTED	121	
DB	75	-----LEEBLTLTKGAKHYIMLFVPTLCMIVVATKSYRFTTEKNGGLITPTED	127	
QY	122	TEIVGORALHSILNAIMISIVYVMTLLVLYKXRCYKVTHAWLLISLLLEFFSFY	181	
DB	128	TPSQGRLNSVLTMLIMISIVYVMTIFLVLYKXRCYKFTHGMIMESIMLLEFFTYIY	187	
QY	182	LGEFPTKTNVAVDYITVALLIMNFGVGMISIMHKGPRLOQAYIMLSALMALVFIKL	241	
DB	188	LGEVLKTYNVAMDPTLLTVMNNGAVGMVCLHMGKPYLQOAYIMLSALMALVFIKL	247	
QY	242	PENTAMLLIAYISYVDIYAVLCLKGPLMLVETAGERNETLLPALLIYSTMYVLVMAEG	301	
DB	248	PENSAWVILGAI SYVDIYAVLCPKGPLMLVETAGERNETLLPALLIYSAMWTVGMKLT	307	
QY	302	DPEAQRKRSKSKNNAESTERESQDTVAENDDGSESEMEQRQSDHLTPHSTPESRAAV	361	
DB	308	DPSSQGAN-QLPDPF-MEEDSYDSFGE---PSIPEVFEPLTGYPC-----	349	
QY	362	QELSSILAGEDPEERGVKLGIDPIFYSVLVGKASATAGDMNTTIACFVAIILGLCLT	421	
DB	350	EDL-----EBEERGVKLGIDPIFYSVLVGKAAAGSGDMNTTIACFVAIILGLCLT	402	
QY	422	LLLLAIFKKALPALPISTITGIVVFAPADYIVQPMQDLAFHQFIY 467		
DB	403	LLLLAVFKKALPALPISTITGIIFFSYDNLVPRPMDLASHQLYI 448		

RESULT 11

PSN2 MICMU

ID PSN2 MICMU

AC P79601

DT 15-JUL-1999 (Rel. 38, Created)

STANDARD

PRT

445 AA.

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Presentin 2 (PS-2) (Fragment).
 GN PSN2 OR PSN2 OR PS2.
 OS Microtus murinus (Lesser mouse Lemur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Cheirogaleidae;
 OC Microtus.
 CX NCBI_Taxid=30608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99167105; PubMed=10069575;
 RA Calenda A., Mestre-Frances N., Czech C., Pradier L., Pelter A.,
 RT Perier M., Bons N., Bellis M.,
 RT "Cloning of the presentin 2 cDNA and its distribution in brain of
 RT the primate, Microtus murinus: coexpression with betaAPP and Tau
 RT proteins." Dis. 5:323-333(1998).
 RL Neurobiol.
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors and
 CC APP (beta-amyloid precursor protein). Requires the other members
 CC of the gamma-secretase complex to have a protease activity. May
 CC play a role in intracellular signaling and gene expression or in
 CC linking chromatin to the nuclear membrane. May function in the
 CC cytoplasmic partitioning of proteins (By similarity).
 CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
 CC complex composed of a presentin homodimer (PSN1 or PSN2),
 CC nicastrin (NCSTN), APH1 (APH1A or APH1B) and PEN2. Such minimal
 CC complex is sufficient for secretase activity, although other
 CC components may exist. Interacts with DOK3. Interacts with
 CC HERPUD1, FLNA and FLNB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 CC endoplasmic reticulum (By similarity).
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Belongs to the presentin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, Y10140, CAA71228.1, -.
 DR MEROPS; A22.002, -.
 DR InterPro; IPR006639; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presentin; 1.
 DR PRINTS; PRO1072; PRESENTIN.
 DR SMART; SM00730; PSN. 1.
 KM Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
 FT CHAIN 1 297 PRESENTIN 2 NTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 1 87 PRESENTIN 2 CTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 88 108 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 109 138 LUMENAL (POTENTIAL).
 FT DOMAIN 139 159 POTENTIAL.
 FT DOMAIN 160 166 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 167 187 POTENTIAL.
 FT DOMAIN 188 200 LUMENAL (POTENTIAL).
 FT DOMAIN 201 221 POTENTIAL.
 FT DOMAIN 222 223 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 224 244 LUMENAL (POTENTIAL).
 FT DOMAIN 245 249 POTENTIAL.
 FT DOMAIN 250 271 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 272 368 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 369 409 POTENTIAL.
 FT TRANSMEM 414 434 POTENTIAL.
 FT NON_TER 445
 FT 445 AA; 49475 MW; 0A01A764659E052 CRC64;

Query Match 60.2%; Score 1440; DB 1; Length 445;
 Best Local Similarity 65.0%; Pred. No. 5e-93;
 Matches 301; Conservative 42; Mismatches 78; Indels 42; Gaps 8;
 QY 3 ELIAPLSTFYQNAQNSDNLNTYRSGQDNREGRSHNDR-SLGHPEPLSGRQGNRSQ 61
 DB 24 ESPSPRSQCEGQGGEDDSTQWRIOQSEEDGEDDPYVSSGPV-----GRPG----- 74
 QY 62 VVEQDEEDDELTLYKGAHYIMLFVPTLGMVVATIKSVSPYTRKQGLIYPTED 121
 DB 75 -----PEEELTKYGAHYIMLSVPTLGMVVATIKSVRYTEKNGOLITPTED 127
 QY 122 TETVQORALSHLNAIMISIVVMTILVLYKRCRYTHANLILSSLLLPFFSRY 181
 DB 128 TPVSQORLNSVLTMLMISIVVMTIFLVLYKRCRYTHGWLIMSLLLPFFYIY 187
 QY 162 LGEVFKTVNAVDTYVTLALIMNFGVGMISIHMKGPLRQAYLIMISALMALVFTKY 241
 DB 168 LGEVLTNTVNAVDTYVTLVTVNNGAVGMVCIHMKGPLMQAYLILASALMALVFTKY 247
 QY 242 PEMTAMLLIAYISYVDLVAVLCLKGPLMLVETAQERNETLFPALITSTWVLVNAEG 301
 DB 248 PEMSAMVILGAIISYVDLVAVLCPKGPLMLVETAQERNETLFPALITSSAMVTVGAKL 307
 QY 302 DPEARRVSKSKNAESTERESQTVLENDDGSESEWEMQRDSHGPHSTESRAV 361
 DB 308 DSSQGL--QLPYDE-MEEDSYSLGE--PSIPEVFAPLPGYP----- 349
 QY 362 CELSSILAGEDEPERGVKLGIDFIYSVLVGNASATASGDMWTTIACFVAIILGLT 421
 DB 350 EEL-----EEERGVKLGIDFIYSVLVGNAAATSGDMWTTIACFVAIILGLT 402
 QY 422 LLLILFFKALPALPISITFGVTFPARDIYVOPMDLAHQ 464
 DB 403 LLLILVFKALPALPISITFGVTFPARDIYVOPMDLAHQ 445
 RESULT 12
 ID PSN2_BOVIN STANDARD. PRT; 449 AA.
 AC Q9X796;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Presentin 2 (PS-2).
 GN PSN2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Sahana N., Shitrasawa T., Mori H.,
 RT "Molecular cloning of bovine presentin 2 gene."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors and
 CC APP (beta-amyloid precursor protein). Requires the other members
 CC of the gamma-secretase complex to have a protease activity. May
 CC play a role in intracellular signaling and gene expression or in
 CC linking chromatin to the nuclear membrane. May function in the
 CC cytoplasmic partitioning of proteins (By similarity).
 CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
 CC complex composed of a presentin homodimer (PSN1 or PSN2),
 CC nicastrin (NCSTN), APH1 (APH1A or APH1B) and PEN2. Such minimal
 CC complex is sufficient for secretase activity, although other
 CC components may exist. Interacts with DOK3. Interacts with
 CC HERPUD1, FLNA and FLNB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:53:51 ; Search time 45 Seconds

(without alignments)
3274.378 Million cell updates/sec

Title: US-09-785-474A-30

Sequence: 1 MTELPAPLPYFQNAQSEDN.....ATDYLQPPMDLAFHQFYI 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1975.5	82.6	468	13 Q90X08	Q90X08 gallus galli
2	1529.5	64.0	384	13 Q73869	Q73869 cyprinus ca
3	1368	57.2	504	5 Q8W558	Q8W558 branchiosteo
4	1361.5	56.9	451	13 Q90X07	Q90X07 gallus galli
5	1360.5	56.9	525	5 Q8W559	Q8W559 branchiosteo
6	1240.5	51.9	582	5 Q9GU38	Q9GU38 helix lucor
7	675	28.2	133	6 Q8WZ65	Q8WZ65 oryctolagus
8	671	28.1	133	6 Q8WZ65	Q8WZ65 oryctolagus
9	532	23.1	133	6 Q8WZ65	Q8WZ65 oryctolagus
10	159	6.6	478	10 Q8ED32	Q8ED32 oryza sativ
11	132.5	5.5	455	16 Q8WZ65	Q8WZ65 oryctolagus
12	120.5	5.0	661	11 Q8WZ65	Q8WZ65 oryctolagus
13	120.5	5.0	691	4 Q9HNS3	Q9HNS3 mus musculu
14	120	5.0	616	5 Q8WZ65	Q8WZ65 oryctolagus
15	118.5	5.0	309	16 Q9HNS3	Q9HNS3 mus musculu
16	118	4.9	555	2 Q8WZ65	Q8WZ65 oryctolagus

17	116.5	4.9	438	16 Q8A257	Q8A257 bacteroides
18	115.5	4.8	606	13 Q70P03	Q70P03 xenopus lae
19	115	4.8	364	16 Q92U24	Q92U24 rhizobium m
20	115	4.8	417	16 Q8RH68	Q8RH68 fusobacteri
21	115	4.8	601	5 Q8WZ65	Q8WZ65 oryctolagus
22	114.5	4.8	754	13 Q8WZ65	Q8WZ65 oryctolagus
23	113	4.7	224	2 Q8WZ65	Q8WZ65 oryctolagus
24	113	4.7	539	16 Q8WZ65	Q8WZ65 oryctolagus
25	112	4.7	321	11 Q70P03	Q70P03 xenopus lae
26	112	4.7	410	2 Q8WZ65	Q8WZ65 oryctolagus
27	111.5	4.7	339	17 Q8WZ65	Q8WZ65 oryctolagus
28	111	4.6	578	2 Q9HNS3	Q9HNS3 mus musculu
29	110	4.6	318	17 Q9HNS3	Q9HNS3 mus musculu
30	110	4.6	540	5 Q8WZ65	Q8WZ65 oryctolagus
31	110	4.6	705	11 Q8WZ65	Q8WZ65 oryctolagus
32	110	4.6	707	10 Q9T050	Q9T050 arabidopsis
33	110	4.6	835	4 Q8WZ65	Q8WZ65 oryctolagus
34	109.5	4.6	379	2 Q8WZ65	Q8WZ65 oryctolagus
35	109.5	4.6	408	13 Q8WZ65	Q8WZ65 oryctolagus
36	109.5	4.6	598	10 Q8WZ65	Q8WZ65 oryctolagus
37	109.5	4.6	838	16 Q8WZ65	Q8WZ65 oryctolagus
38	109	4.6	539	5 Q22089	Q22089 caenorhabdi
39	108	4.5	3374	12 Q8WZ65	Q8WZ65 oryctolagus
40	107.5	4.5	590	6 Q8WZ65	Q8WZ65 oryctolagus
41	107.5	4.5	699	10 Q93Z05	Q93Z05 canis famli
42	107	4.5	813	5 Q8WZ65	Q8WZ65 oryctolagus
43	106.5	4.5	571	13 Q8WZ65	Q8WZ65 oryctolagus
44	106	4.4	269	2 Q9WYX0	Q9WYX0 pedicoccus
45	106	4.4	515	16 Q8WZ65	Q8WZ65 oryctolagus

ALIGNMENTS

RESULT 1	Q90X08	PRELIMINARY;	PRT;	468 AA.
AC	Q90X08;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Presentin 1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_Taxid=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRALINE4; TISSUE=Brain;			
RC	Korade Mirnics Z., Keryanov S., Lovelock J., Corey S.J.;			
RT	"Cloning of chicken presentinins."			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY043492; AAX95408.1; -			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	InterPro; IPR006639; Peptidase_A22.			
DR	InterPro; IPR001108; Peptidase_A22A.			
DR	Pfam; PF01080; Presentin_1.			
DR	PRINTS; PRO1072; PRESENTIN.			
DR	SMART; SM00730; PSN.1.			
DR	SEQUENCE 468 AA; 52812 MW; B746BEDA3BAC0BPA CRC64;			
Qy	Query Match	82.6%;	Score 1975.5;	DB 13; Length 468;
Qy	Best Local Similarity	83.1%;	Pred. No. 5.2e-156;	
Qy	Matches 392;	Conservative 30;	Mismatches 41;	Indels 9; Gaps 3;
Db	1 MTELPAPLPYFQNAQSEDN---DNHLSNTVRSQNDNRROSH--NDRSLGHPPLSNGRP 55			
Qy	1 MTELPAPLPYFQNAQSEDN---DNHLSNTVRSQNDNRROSH--NDRSLGHPPLSNGRP 55			
Qy	56 QGNSRQVEODEDEDELTITKYGAKAVITLFPVYTLQMTVVATITISVSYYTRKQGLIT 115			

Db 57 QNNIQVVDQDEDEDELLTKYGAKHIMLFPVTLQMVVAVATIKSVSYTRKQGLY 116
 QY 116 TPTEDETEVGORALSHIINAAIMISYIVVMTLLVLYKRCYKVIHAMIILSSLLLF 175
 Db 117 TPTEDETEVGORALSHIINAAIMISYIVVMTLLVLYKRCYKVIHAMIILSSLLLF 176
 QY 176 FFSFIYGEVFKTVNAVADYITVALLIMNFGVGMISIMHKGPIRLQOAVLIMISALML 235
 Db 177 FFSFIYGEVFKTVNAVADYITVALLIMNFGVGMISIMHKGPIRLQOAVLIMISALML 236
 QY 236 VFIKLPEMTMLIAVSVYDLVAVLCLKGLPLMVELTAOERNETLFPALISSTVWL 235
 Db 237 VFIKLPEMTMLIAVSVYDLVAVLCLKGLPLMVELTAOERNETLFPALISSTVWL 236
 QY 236 VNMAGEDEAQRVSKNSKNAESTERESQDTVAENDDGGFSEEMEAQRSDHGLGPRSTP 355
 Db 237 VNMAGEDEAQRVSKNSKNAESTERESQDTVAENDDGGFSEEMEAQRSDHGLGPRSTP 356
 QY 356 ESRAVVOELSSILLAGEPBERGVGLGDFIFYSVLVGKASATASGDMNTTIACFVAL 415
 Db 357 ESRAVVOELSSILLAGEPBERGVGLGDFIFYSVLVGKASATASGDMNTTIACFVAL 416
 QY 416 IGLCTLLLLAIFKKALPALPISITFGLVFFATDYLVPFMDQLAFHOFYI 467
 Db 417 IGLCTLLLLAIFKKALPALPISITFGLVFFATDYLVPFMDQLAFHOFYI 468

RESULT 2

073869 PRELIMINARY; PRT; 384 AA.
 ID 073869
 AC 073869
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PSI protein (Fragment).
 GN PSI.
 OS *Cyprinus carpio* (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OC NCBI_TaxID=962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337349; PubMed=9674592;
 RA Archer S., Hirano J., Dies J.K.J., Fraser S.P., Djamgoz M.B.A.;
 RT "Expression and localization in the fish retina of a homologue of the
 RT Alzheimer's related psi gene."
 RT Alzheimer's related psi gene.
 RT Neuroreport 9:2049-2056 (1998).
 RL EMBL: Y17128; CAA/6641.1; --
 DR MEROPS; A22.001; --
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR006639; Peptidase A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presentinlin. 1.
 DR PRINTS; PRO1072; PRESENTLIN.
 DR SMART; SM00730; PSN; 1.
 FT NON TER 1
 FT VARIANT 5 5 I -> V.
 FT VARIANT 56 56 A -> S.
 FT VARIANT 56 56 A -> V.
 FT VARIANT 60 60 S -> G.
 FT VARIANT 63 63 V -> L.
 FT VARIANT 83 83 G -> A.
 FT VARIANT 83 83 A -> S.
 FT VARIANT 118 118 P -> T.
 FT VARIANT 200 200 P -> T.
 SQ SEQUENCE 384 AA; 43276 MW; F97BEFE24B31FDAA CRC64;

Query March 64.0%; Score 1529.5; DB 13; Length 384;
 Best Local Similarity 79.5%; Pred. No. 5.6e-119;
 Matches 311; Conservative 27; Mismatches 40; Indels 13; Gaps 6;
 QY 83 IMLFVPTLCMVVVAVATIKSVSYTRKDG-QLITPTEDETEVGORALSHIINAAIMIS 141

Db 1 IMLFVPTLCMVVVAVATIKSVSYTRKDGQGLITPTEDETEVGORALSHIINAAIMIS 60
 QY 142 VIVVMTLLVLYKRCYKVIHAMIILSSLLLFPSFIYGEVFKTVNAVADYITVALL 201
 Db 61 VIVVMTLLVLYKRCYKVIHAMIILSSLLLFPSFIYGEVFKTVNAVADYITVALL 120
 QY 202 IMNFGVGMISIMHKGPIRLQOAVLIMISALMALVFIKLPEMTMLIAVSVYDLVAV 261
 Db 121 IMNFGVGMISIMHKGPIRLQOAVLIMISALMALVFIKLPEMTMLIAVSVYDLVAV 180
 QY 262 LCLKGLPLMVELTAOERNETLFPALISSTVWLNMAGEDEAQRVSKNSKNAESTE 321
 Db 181 LCLKGLPLMVELTAOERNETLFPALISSTVWLNMAGEDEAQRVSKNSKNAESTE 233
 QY 322 RESQDTVA---ENDDGGFSEEMEAQRSDHGLGPRSTPESRAVVOELSSILLAG-EDPEE 376
 Db 234 QENQDAVAPTAQPEDDGGFTPAVNVNQCHQLPQSTEDSKREIQLTSARPPVEDDE 293
 QY 377 RGVLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCTLLLLAIFKKALPALP 436
 Db 294 RGVLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCTLLLLAIFKKALPALP 353
 QY 437 ISTFGLVFFATDYLVPFMDQLAFHOFYI 467
 Db 354 ISTFGLVFFATDYLVPFMDQLAFHOFYI 384

RESULT 3

08WS58 PRELIMINARY; PRT; 504 AA.
 ID 08WS58
 AC 08WS58
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Presentinlin.
 GN PS.
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OC NCBI_TaxID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21590369; PubMed=11733140;
 RA Martinez-Mir A., Caneiro C., Gonzalez-Duarte R., Albalat R.;
 RT "Characterization of the amphioxus presentin gene in a high gene-
 RT density genomic region illustrates duplication during the vertebrate
 RT lineage."
 RT lineage.
 RT Gene 279:157-164 (2001).
 RL EMBL: AF369891; AAL40416.1; JOINED.
 DR EMBL; AF369890; AAL40416.1; --
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008447; HTH_LysR.
 DR InterPro; IPR006639; Peptidase A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presentinlin. 1.
 DR PRINTS; PRO1072; PRESENTLIN.
 DR SMART; SM00730; PSN; 1.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
 SQ SEQUENCE 504 AA; 55443 MW; 9C3794D030285984 CRC64;

Query March 57.2%; Score 1368; DB 5; Length 504;
 Best Local Similarity 58.8%; Pred. No. 2.2e-105;
 Matches 275; Conservative 56; Mismatches 101; Indels 36; Gaps 7;
 QY 27 RSGQDNREKQSHNDRSIGHEPLSNRPGQNSGVVQDEDEDETEITKYGAKHIMLFP 86
 Db 46 RSGQDNREKQSHNDRSIGHEPLSNRPGQNSGVVQDEDEDETEITKYGAKHIMLFP 98
 QY 87 VPTLCMVVVAVATIKSVSYTRKDGQGLITPTEDETEVGORALSHIINAAIMISVIVM 146

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Db 99 AVSLCMAVVAATISSITTEKNGLYITPHEBASTASVGSISANGALMGVILVM 158
147 TLILVVLKYRCYKVHAWLIISLLLFPSFIYLGVEFKTYNAVDYITVALLIMNG 206
159 TVFLVLVLYKRCYKCFHGMWLIISLMLFLFAYIYLGVTLCQAVNIPCDYITLAIWMNG 218
207 VVGMIISHWKGPRLQOAVLIMISALMALVFIKYLPENTAMVILAVISYDVAVLCCKG 266
219 AVGMCIHWKGPRLQOAVLIMISALMALVFIKYLPENTAMVILAVISYDVAVLCCKG 278
267 PLRMLVETAOENNETLFPALITVSTVWLVNNAEDPEARVSKSKNAESTERES-- 324
279 PLKVLVETAOENNETLFPALITVSTVWLVNNAEDPEARVSKSKNAESTERES-- 338
325 -QDTVAENDDGGFSEMEAR--DSHLGPHR-----STPERAAVQELSSILA-- 370
339 PAGAVGEEGEGFGPMNESRGOPTRFRNRCGNASDASVNSEDAKQAQNLNRSRSPS 398
371 -----GDPBERGVKLGLDPIFYSVLVKASATNSGDWNTTIACFVAILIGLC 419
399 GNGOQOQWEEDEDEBERGVKLGLDPIFYSVLVKAS--SNGDWNITLACFVAILIGLC 456
420 LTLILALFKKALPALPISITGVLVFPATDVLQPFMDLAFHGPYI 467
457 LTLILALFKKALPALPISITGVLVFPATDVLQPFMDLAFHGPYI 504

```

RESULT 4

```

O90X07 PRELIMINARY: PRT: 451 AA.
ID O90X07:
AC 090X07:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Presentin. 2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RA Korde Mirice Z., Kervanov S., Lovelock J., Corey S.J.,
RT "Cloning of chicken presentin."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF043493; AAK95409.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR001108; Peptidase_A22A.
DR Pfam; PRO1080; Presentin_1.
DR PRINTS; PRO1072; PRESENTIN.
DR SMART; SM00730; PSN; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
SQ SEQUENCE 451 AA; 50456 MW; 534E6364C627E8B0 CRC64;

```

Query Match 56.9%; Score 1361.5; DB 13; Length 451;
 Best Local Similarity 59.7%; Pred. No. 6.6e-105;
 Matches 283; Conservative 43; Mismatches 71; Indels 77; Gaps 7;

```

QY 3 ELPAFLSTFQNAQWSEDNHLSNTVRSQNDNRERQHNDRSLGHEPLNSGRPOGNSR-- 60
DB 25 EEPFVPSYODGLQASE-----TREAQTHRRKQT-----GSSRSP 58
QY 61 -QVNVOD-----EEDEELTKYKAKVIMLFVPTLLCMVVAATIKSVSY 106
DB 59 NNVADEBDSQVYRRESALENEEBELTLKYGAKVIMLFVPTLLCMVVAATIKSVRFY 118
QY 107 TRKQGLIYTPPTEDTEVQGRALHSINAAIMSVIWMVILLVLYKRCYKVIHAWL 166
DB 119 TEKNQGLIYTPPTEDTEVQGRALHSINAAIMSVIWMVILLVLYKRCYKVIHAWL 178
QY 167 IISLILFFPSFIYLGVEFKTYNAVDYITVALLIMNGVGMISHWKGPRLQOAVL 226

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Db 179 ILSFMLIFPTIYLYGAEVKTYNVANDYPTVLLINFGAVGIRIHWKGPRLQOAVL 238
QY 227 IMISALMALVFIKYLPENTAMVILAVISYDVAVLCCKGPLMLVETAOENNETLFPAL 286
Db 239 IMISALMALVFIKYLPENTAMVILAVISYDVAVLCCKGPLMLVETAOENNETLFPAL 298
QY 267 IYSSTWLVNNAEGDEPEARVSKSKNAESTERESQDTVAENDDGGFSEMEARQDS 346
Db 299 IYSSTWLVNNAEGDEPEARVSKSKNAESTERESQDTVAENDDGGFSEMEARQDS 391
QY 347 HLGPHRSTPERAAVQELSS-----ILAGDPBERGVKLGLDPIFYSVLVKASATA 400
Db 332 E--NHSSTSDSQIIDTRPAPSHPTLEMEBERGVKLGLDPIFYSVLVKASATA 389
QY 401 SGDMNTTILACFVAILIGLCITLILALFKKALPALPISITGVLVFPATDVLQ 454
Db 390 SGDMNTTILACFVAILIGLCITLILALFKKALPALPISITGVLVFPATDVLQ 443

```

RESULT 5

```

O8WS59 PRELIMINARY: PRT: 525 AA.
ID O8WS59:
AC O8WS59:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Presentin.
GN PS.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomida;
OC Branchiostoma.
RX NCBI_TaxID=7739;
RN (1)
RP SEQUENCE FROM N.A.
RA Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.,
RT "Characterization of the amphioxus presentin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RL Gene 279;157-164(2001).
DR EMBL; AF369891; AAL40414.1; -.
DR EMBL; AF369890; AAL40414.1; JOINED.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_Ly68.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR001108; Peptidase_A22A.
DR Pfam; PRO1080; Presentin_1.
DR PRINTS; PRO1072; PRESENTIN.
DR SMART; SM00730; PSN; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
SQ SEQUENCE 525 AA; 57598 MW; 2B14CF77A80F07DE CRC64;

```

Query Match 56.6%; Score 1360.5; DB 5; Length 525;
 Best Local Similarity 56.6%; Pred. No. 9.6e-105;
 Matches 277; Conservative 56; Mismatches 99; Indels 57; Gaps 8;

```

QY 27 RQNDNRERQHNDRSLGHEPLNSGRPOGNSRQVYEDDEEBELTLKYGAKVIMLF 86
Db 46 RQNDNRERQHNDRSLGHEPLNSGRPOGNSRQVYEDDEEBELTLKYGAKVIMLF 98
QY 87 VPTLLCMVVAATIKSVSYTRKQGLIYTPPTEDTEVQGRALHSINAAIMSVIWMV 146
Db 99 AVSLCMAVVAATISSITTEKNGLYITPHEBASTASVGSISANGALMGVILVM 158
QY 147 TLILVVLKYRCYKVHAWLIISLLLFPSFIYLGVEFKTYNAVDYITVALLIMNG 206
Db 159 TVFLVLVLYKRCYKCFHGMWLIISLMLFLFAYIYLGVTLCQAVNIPCDYITLAIWMNG 218
QY 207 VVGMIISHWKGPRLQOAVLIMISALMALVFIKYLPENTAMVILAVISYDVAVLCCKG 266

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Db      219 AVGVGCIHMKGPILLQQAIVLIVISALMALVFIKLPWTWFLTGAISTYDLAVAVLCPK 278
QY      267 PLRLVETAEORNETLFPALISSTWMLVYMAEGDEAQRVSKNSKHAE----- 319
Db      279 PLKLVETAEORNETLFPALISSTWMLVYMAEGDEAQRVSKNSKHAE----- 319
QY      320 ---TERESQDT-----VAENDGGESEWEAQR--DSHLGHR----- 352
Db      339 FRLLNDAGSGTGDDADAFDAPAGAVGSEEGGFGPWNESRGPQTRRNRGASDAS 398
QY      353 -STPESRAVVOELSSSILA-----GSDPEERGVKLGDFIFYSVLVKGASA 398
Db      399 VNSHDAQAQNLNSGRSLSPSGNQOQOQMEDEDEBERGVKLGDFIFYSVLVKGAS- 457
QY      399 TASGDWNTTACFAVAILIGLCTLLLAIFKKALPALPISITGLVFPFATDYLVOPEMD 458
Db      458 -SNGDMWNTTACFAVAILIGLCTLLLAIFKKALPALPISITGLVFPFATDYLVOPEMD 516
QY      459 QLAHFQFYI 467
Db      517 ALASQVYV 525

RESULT 6
Q9GU38 PRELIMINARY; PRT; 582 AA.
ID Q9GU38
AC Q9GU38;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Presentinlin.
GN PS.
OS Helix lucorum.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidae; Helicidae; Helix.
OX NCBI_TaxID=31229;
RN (1)
RA SEQUENCE FROM N.A.
RA Rogaev E.I., Riazanskaya N.N., Dvorlanchikov G., Grigorenko A.P.,
RA Tyrsin O.;
RT "Presentinlin gene isolated from mollusk Helix lucorum."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF197861; AAC28518.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro: IPR006639; Peptidase_A22.
DR InterPro: IPR001108; Peptidase_A22A.
DR Pfam: PF01080; Presentinlin; 1.
DR PRINTS: PRO1072; PRESENTLIN.
DR SMART: SMO0730; PSN; 1.
FT NON_TER
SQ SEQUENCE 582 AA; 63782 MW; 07934E7C452199F0 CRC64;

Query Match 51.9%; Score 1240.5; DB 5; Length 582;
Best Local Similarity 48.1%; Pred. No. 1.1e-94;
Matches 267; Conservative 73; Mismatches 108; Indels 107; Gaps 11;

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QY      225 LVFIKYLEPNTAWLILAVISYVDLVAVLCLKGPIRLVETAQRNETLFPALISSTWMLV 294
Db      222 LMFIRYTDWNTWAVLGVMTVDLVAVLCFPGPIRLVETAQRNETLFPALISSTWMLV 331
QY      295 LVNMAEGDEAQRVSKNSKHAE-----VAENDGGESEWEAQR--DSH 347
Db      332 FVTMADDDGQKKQKKKGTGAQNSSVTTPGKGT--DDDGGFTEHVAANGTQHS 389
QY      348 LGRHSTPESRAVVOEL-----SSILAGE----- 373
Db      390 LTASQDSQARRNAVQAFDMVQDKPRDRNAVSHTTVNTNSARVLATKDGAVESAVR 449
QY      374 -----PEERGVKLGDFIFYSVL 392
Db      450 VNVQORDAVVANSRQNSRTRPALQRRPLDSDSINQDDEBERGVKLGDFIFYSVL 509
QY      393 VGRASATASGWNNTTACFAVAILIGLCTLLLAIFKKALPALPISITGLVFPFADYL 452
Db      510 VGRAS--SNGDMWNTTACFAVAILIGLCTLLLAIFKKALPALPISITGLVFPFATSSL 567
QY      453 VQPEMDQLAFHOFYI 467
Db      568 VQPEMDQLAFHOFYI 582

RESULT 7
Q8H266 PRELIMINARY; PRT; 133 AA.
ID Q8H266
AC Q8H266;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Presentinlin-1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RA SEQUENCE FROM N.A.
RA Al-Khedhairy A.A., Arfin M., Al-Dukhyi A.B.;
RT "Molecular cloning and sequencing of the rabbit presentinlin-1 cDNA
RT fragment."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY134851; AAN08438.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro: IPR006639; Peptidase_A22.
DR InterPro: IPR001108; Peptidase_A22A.
DR Pfam: PF01080; Presentinlin; 1.
DR SMART: SMO0730; PSN; 1.
FT NON_TER
SQ SEQUENCE 133 AA; 15398 MW; F79114407D741226 CRC64;

Query Match 28.2%; Score 675; DB 6; Length 133;
Best Local Similarity 98.5%; Pred. No. 2.1e-48;
Matches 131; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      9 SYFQNAQMSDNHLSNTV-----RSQDNREKROHNRRLGHPPLS-----NKR 54
Db      39 SRYSLSLQMSLTDVV-NAVPEATVDPKSGDASSRSGNNSRQCVTSQASERRAPNNE 97
QY      55 POGNSRQVQDEDEDEDELTKYGAQKAVIMLFVPTLVCMVVVVATIKSVFYTRKQGOI 114
Db      98 PSGGN-----QDEDDDEE-TLLYGAQKAVIMLFVPTLVCMVVVVATIKSVFYTRKQGOI 151
QY      115 YTPTEDEPTVYQORALHSILNAAIMISYIVMTLLVLYKRCYKVIHMLISSLILL 174
Db      152 YTPTEDEPTVYQORALHSILNAAIMISYIVMTLLVLYKRCYKVIHMLISSLILL 211
QY      175 FFFSFIYLGVEFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQQAIVLIMISALMA 234
Db      212 FFFSFIYLGVEFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQQAIVLIMISALMA 271

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QY      112 QLIYTFPEDEPTVYQORALHSILNAAIMISYIVMTLLVLYKRCYKVIHMLISSLILL 171
Db      1 QLIYTFPEDEPTVYQORALHSILNAAIMISYIVMTLLVLYKRCYKVIHMLISSLILL 60
QY      172 LLLPFSFIYLGVEFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQQAIVLIMISA 231
Db      61 LLLPFSFIYLGVEFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQQAIVLIMISA 120
QY      232 LMAVFIKYLEP 244
Db      121 LMAVFIKYLEP 133

RESULT 8
Q8H265

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:49:57 ; Search time 60 Seconds

(without alignments)
2199.161 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391

Sequence: 1 MTELPAPISYFQNAQMSEDN.....ATDYLVQFMDQLAFHOFYI 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	99.7	467	2	AAW05751 Present11
2	2384	99.7	467	2	AAW27176 Human S18
3	2378	99.5	467	2	AAW05733 Present11
4	2378	99.5	467	2	AAW41430 Present11
5	2378	99.5	467	2	AAW23864 Human pre
6	2378	99.5	467	2	AAW24419 Human pre
7	2378	99.5	467	2	AAW23897 Human pre
8	2378	99.5	467	3	AAW07971 Amino aci
9	2378	99.5	467	4	AAW10798 Human pre
10	2378	99.5	467	4	AAW63936 Amino aci
11	2378	99.5	467	4	AAW05466 Human pre
12	2378	99.5	467	5	AAW17051 Human pre
13	2378	99.5	467	5	AAW17916 Human pre
14	2378	99.5	467	5	AAW18049 Present11
15	2375	99.3	467	2	AAW05737 Present11
16	2375	99.3	467	2	AAW05755 Present11
17	2375	99.3	467	2	AAW05758 Present11
18	2375	99.3	467	2	AAW05754 Present11
19	2374	99.3	467	2	AAW05749 Present11
20	2374	99.3	467	2	AAW05747 Present11
21	2374	99.3	467	2	AAW05736 Present11
22	2374	99.3	467	2	AAW27177 Human mut
23	2374	99.3	467	4	AAW05563 Human pre
24	2373	99.2	467	2	AAW05746 Present11
25	2373	99.2	467	2	AAW05738 Present11

26	2373	99.2	467	2	AAW05748 Present11
27	2373	99.2	467	2	AAW05739 Present11
28	2373	99.2	467	2	AAW05741 Present11
29	2372	99.2	467	2	AAW05753 Present11
30	2372	99.2	467	2	AAW05740 Present11
31	2372	99.2	467	2	AAW05742 Present11
32	2372	99.2	467	2	AAW05757 Present11
33	2371	99.2	467	2	AAW05744 Present11
34	2371	99.2	467	2	AAW6770 Homo sapi
35	2371	99.2	467	4	AAW05564 Human pre
36	2370	99.1	467	2	AAW05752 Present11
37	2369	99.1	467	2	AAW05743 Present11
38	2369	99.1	467	2	AAW05745 Present11
39	2368	99.0	467	5	AAW17045 Human mut
40	2367	99.0	467	2	AAW05759 Present11
41	2366	99.0	467	2	AAW05750 Present11
42	2366	99.0	467	5	AAW17046 Human mut
43	2357	98.6	465	3	AAW51393 Human S18
44	2357	98.6	467	2	AAW1839 Human ear
45	2356	98.5	467	5	AAW17047 Human mut

ALIGNMENTS

RESULT 1
AAW05751
ID AAW05751 standard; protein; 467 AA.
XX
AC AAW05751;
XX
DT 25-MAR-2003 (revised)
DT 23-JUL-1997 (first entry)
XX
DE Present11-1-1 P264L mutation.
XX
KW Present11-1; human; hps1-1; hps1-2; PS-2; Integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; muten.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 264 /label= P264L
XX
XX
XX NO9634099-A2.
XX
XX 31-OCT-1996.
XX
XX 29-APR-1996; 96WO-CA000263.
XX
XX 28-APR-1995; 95US-00431048.
XX 28-JUN-1995; 95US-00496841.
XX 31-JUL-1995; 95US-00503359.
XX
XX (HSCR-) HSC RES & DEV LP.
XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
XX St George's Hosp PH, Fraser PE, Rommens JM;
XX WPI; 1996-497631/49.
XX
XX New present11 genes - useful for diagnosis, therapy and drug screening
XX of familial Alzheimer's disease, cerebral disorders, etc.
XX
XX Claim 3; Page; 178pp; English.
XX
XX AAW05736-W05760 represent mutated versions of the human present11-1-1
XX protein (see AAW05733 for wild type sequence). AAW05734 represents a
XX different wild type form of present11-1 that results from alternate
XX splicing of the genomic DNA sequence. The present11s are a family of
XX highly conserved integral membrane proteins with a common structural

CC motif, common alternate splicing patterns, and common mutational hot spot
 CC regions. Mutations in PS genes are implicated in familial Alzheimer's
 CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
 CC schizophrenia, depression etc., so detection of mutations in the DNA
 CC encoding the wild type sequences can be used for diagnosis of these
 CC diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are useful
 CC as models for drug screening. The antibodies can also be used e.g. for
 CC affinity purification and in immunoassays. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 XX

SO Sequence 467 AA;

Query Match 99.7%; Score 2385; DB 2; Length 467;
 Best Local Similarity 99.8%; Pred. No. 2,76-234;
 Matches 466; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNRPGQNSR 60
 DB 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNRPGQNSR 60
 QY 61 QVEODEEDEDDELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYRKQGLIYTPFTE 120
 DB 61 QVEODEEDEDDELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYRKQGLIYTPFTE 120
 QY 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQQAAYLIMISALMAVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQQAAYLIMISALMAVFIKY 240
 QY 241 LPENTAMLLAVISYVDLVAVLCKGPLRLMVEAQRNETLFPALYYSTMTWLVNMAE 300
 DB 241 LPENTAMLLAVISYVDLVAVLCKGPLRLMVEAQRNETLFPALYYSTMTWLVNMAE 300
 QY 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 DB 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 QY 361 VOELSSSIILAGEDEERGVKLGDFTFYSVLVKAATASGDMNTTIACFVAIILIGLCL 420
 DB 361 VOELSSSIILAGEDEERGVKLGDFTFYSVLVKAATASGDMNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467

RESULT 2

AAW27176 ID AAW27176 standard; protein; 467 AA.

XX AAW27176;

XX 09-DEC-1997 (first entry)

DE Human S182 gene, PS1 locus, product related to Alzheimer's disease.

XX Mutant; antisense; antibody; vaccine; Alzheimer's disease.

OS Homo sapiens.

XX WO9708319-A1.

XX 06-MAR-1997.

XX 03-SEP-1996; 96WO-US014114.

XX 31-AUG-1995; 95US-0003054P.

PR 30-AUG-1996; 96US-00706344.

XX (GENO) GEN HOSPITAL CORP.

XX Tanzi RE, Masco W;

XX WPI; 1997-179276/16.

DR N-PSDB; AAT85332.

PT Chromosome 14 early-onset familial Alzheimer's disease gene PS1 mutants -
 useful for diagnosing likelihood of developing Alzheimer's disease, also
 anti-sense sequences, antibodies and vaccines to delay onset.

XX Claim 12; Page 72-73; 99p; English.

The present sequence represents the human S182 gene, PS1 locus, product.
 CC Mutant PS1 produces a gene product that increases the probability of
 CC Alzheimer's disease. A nucleic acid sequence able to hybridise to
 CC sequences coding for a mutant PS1 polypeptide can be used as probes for
 CC diagnosing an increased likelihood of contracting Alzheimer's disease.
 CC Antibodies against the mutant polypeptide can also be used for this
 CC purpose. Vectors containing or expressing a nucleic acid molecule,
 CC protein or antibody specific for mutant PS1 can be administered to a
 CC patient to reduce the likelihood, or delay the onset, of Alzheimer's
 CC disease. e.g. anti-sense RNA expression can be used to decrease
 CC expression of the PS1 peptide. Transgenic animals expressing the
 CC Alzheimer's disease protein can be used to test candidate therapeutics
 CC and to investigate the normal role of PS1. The PS1 peptide may also be
 CC included in pharmaceutical compositions (vaccines) for Alzheimer's
 CC disease therapy

SO Sequence 467 AA;

Query Match 99.7%; Score 2384; DB 2; Length 467;
 Best Local Similarity 99.8%; Pred. No. 3,46-234;
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNRPGQNSR 60
 DB 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNRPGQNSR 60
 QY 61 QVEODEEDEDDELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYRKQGLIYTPFTE 120
 DB 61 QVEODEEDEDDELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYRKQGLIYTPFTE 120
 QY 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVVGQRALHSINAAIMSVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQQAAYLIMISALMAVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQQAAYLIMISALMAVFIKY 240
 QY 241 LPENTAMLLAVISYVDLVAVLCKGPLRLMVEAQRNETLFPALYYSTMTWLVNMAE 300
 DB 241 LPENTAMLLAVISYVDLVAVLCKGPLRLMVEAQRNETLFPALYYSTMTWLVNMAE 300
 QY 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 DB 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 QY 361 VOELSSSIILAGEDEERGVKLGDFTFYSVLVKAATASGDMNTTIACFVAIILIGLCL 420
 DB 361 VOELSSSIILAGEDEERGVKLGDFTFYSVLVKAATASGDMNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467

RESULT 3

AAW05733 ID AAW05733 standard; protein; 467 AA.

XX AC AAM05733;
 XX AC 25-MAR-2003 (revised)
 DT 23-JUL-1997 (first entry)
 XX DE Presentin-1-1.
 XX KM Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KM familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy.
 XX OS Homo sapiens.
 XX PN MO9634099-A2.
 PD 31-OCT-1996.
 PF 29-APR-1996; 96WO-CA000263.
 XX PR 28-APR-1995; 95US-00431048.
 PR 28-JUN-1995; 95US-00496841.
 PR 31-JUL-1995; 95US-00509359.
 XX PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 XX PI St George's Hospital, Fraser PE, Rommens JM;
 DR WPI, 1996-497631/49.
 DR N-PSDB; AAT140028.
 XX PT New presentin genes - useful for diagnosis, therapy and drug screening
 PT of familial Alzheimer's disease, cerebral disorders, etc.
 XX BS Claim 2; Page 128-130; 178pp; English.
 CC AAM05733 and AAM05734 represent the two different forms of wild type
 CC human presentin-1 (PS-1). The form represented by AAM05734 results from
 CC alternate splicing of the genomic DNA sequence. AAM05762 represents the
 CC coding sequence for wild type human PS-2. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot spot
 CC regions. Mutations in PS genes are implicated in familial Alzheimer's
 CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
 CC schizophrenia, depression etc., so detection of mutations in the DNA
 CC encoding these sequences can be used for diagnosis of these diseases.
 CC These proteins, or vectors that express them or containing antisense
 CC sequences, antibodies selective for mutant forms of these proteins (such
 CC as AAM05736) and modulators of PS gene expression are potentially useful
 CC for treatment of AD etc. Transgenic animals are useful as models for drug
 CC screening. The antibodies can also be used e.g. for affinity purification
 CC and in immunoassays. (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1,46-233;
 Matches, 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNMQSEEDNLSNTVRSQNDNRROSHNRSLGHPLEPLSNRPOQNSR 60
 DB 1 MTELPAPLSTYFQNMQSEEDNLSNTVRSQNDNRROSHNRSLGHPLEPLSNRPOQNSR 60
 QY 61 QVVEQDEDEBELTLTKGAKVIMLFVPVTLQWVVAVATIKSVFYTRKDGQIYPTFE 120
 DB 61 QVVEQDEDEBELTLTKGAKVIMLFVPVTLQWVVAVATIKSVFYTRKDGQIYPTFE 120
 QY 121 DTEVGGORALHSINMAIMTSIVIVMTLLVLYKYKCYVIAHMLITSLILFFPSFI 180
 DB 121 DTEVGGORALHSINMAIMTSIVIVMTLLVLYKYKCYVIAHMLITSLILFFPSFI 180
 QY 121 DTEVGGORALHSINMAIMTSIVIVMTLLVLYKYKCYVIAHMLITSLILFFPSFI 180
 DB 121 DTEVGGORALHSINMAIMTSIVIVMTLLVLYKYKCYVIAHMLITSLILFFPSFI 180
 QY 181 YLGEVFRTYVAVADYITVALLINFGVGNISIMHKGPELQOAYLIMISALMALVFIKY 240

DB 181 YLGEVFRTYVAVADYITVALLINFGVGNISIMHKGPELQOAYLIMISALMALVFIKY 240
 QY 241 LPEWTAMLLIAVSYVDLVAVLCLKGPLRMLVETAOERNTLFPALIIYSTWVLYNMAE 300
 DB 241 LPEWTAMLLIAVSYVDLVAVLCLKGPLRMLVETAOERNTLFPALIIYSTWVLYNMAE 300
 QY 301 GDEPACRVSKNKNAESTERESQPTVAENDCGFSEWEAORDSHLGPHRSTPSRAA 360
 DB 301 GDEPACRVSKNKNAESTERESQPTVAENDCGFSEWEAORDSHLGPHRSTPSRAA 360
 QY 361 VOELSSSILAGDEPBERGVKLGLDPTFYSVLVKAASATPSGDMNTTACFVAIILGLCL 420
 DB 361 VOELSSSILAGDEPBERGVKLGLDPTFYSVLVKAASATPSGDMNTTACFVAIILGLCL 420
 QY 421 TLILLAIFFKALPALPISITFGLVFEYFATDYLVQPMQDLAFHOEYI 467
 DB 421 TLILLAIFFKALPALPISITFGLVFEYFATDYLVQPMQDLAFHOEYI 467

RESULT 4
 AAM41430
 ID AAM41430 standard; protein; 467 AA.
 XX AC AAM41430;
 DT 04-JUN-1998 (first entry)
 XX DE PS1/467 protein.
 XX KM Presentin peptide; PS1/429; immunogen; immune response; PS1 gene;
 KM Alzheimer's disease; mitochondrial pathology; neurodegeneration;
 KW apoptosis; PS1/467.
 XX OS Homo sapiens.
 XX PN MO9746678-A1.
 PD 11-DEC-1997.
 XX PF 03-JUN-1997; 97WO-US009272.
 XX PR 06-JUN-1996; 96US-00659296.
 PR 18-JUL-1996; 96US-00683315.
 XX PA (FAR) BAYER CORP.
 XX PI Davis UN, Chisholm JC, Drache B;
 XX DR WPI; 1998-042186/04.
 DR N-PSDB; AAV17358.
 XX PT DNA encoding presentin peptide PS1/429 and its analogues - useful for
 PT diagnosis and treatment of Alzheimer's disease.
 XX PS Claim 7; Fig 2; 77pp; English.

This sequence is the PS1/467 presentin peptide. This sequence is
 specifically stated as not being in the nucleic acid of the invention,
 CC which encodes the PS1/429 presentin peptide PS1/429 (II). Cells
 CC transformed with the DNA are used to produce recombinant (II) and
 CC analogues, useful e.g. as immunogens for generating an immune response
 CC against PS1/429. (II) is a new product of the PS1 gene, mutations in
 CC which cause Alzheimer's disease (AD). The nucleic acids are generally
 CC useful as probes for detection and quantification of PS1/429,
 CC particularly for diagnosis of AD, especially the target sequences that
 CC hybridise with probes are isolated for sequencing. Antibodies (Ab) can
 CC also be diagnosed at the protein level using Ab as immunoassay reagents.
 CC Ab can also be used to identify epitopes and for affinity purification of
 CC peptides. Antisense nucleic acid may also be used to regulate expression
 CC of the PS1/429 gene, and both nucleic acids and peptides are useful as
 CC size markers in electrophoresis, chromatography etc. The transgenic
 CC animals are used as models for AD, e.g. for testing drugs. Regulators of

CC the P91/429 gene or polypeptide can be used to treat e.g. AD or diseases
 CC involving mitochondrial pathology, apoptosis and neurodegeneration.
 CC Typical regulators are antisense sequences, ribozymes, aptamers,
 CC synthetic or natural compounds. (II) may also be used to target other
 CC coding sequences to particular cellular locations
 XX

Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQNSDNLNTVRSQNDNRERQNDNRSLGHEPLISNGRPOGNSR 60
 Db 1 MTELPALSYFQNAQNSDNLNTVRSQNDNRERQNDNRSLGHEPLISNGRPOGNSR 60
 QY 61 QVVEODEEDELTKYGAHVIMLPVPTLCVVAVATIKSVFTKDGQILTPTE 120
 Db 61 QVVEODEEDELTKYGAHVIMLPVPTLCVVAVATIKSVFTKDGQILTPTE 120
 QY 121 DTEVGRALHSILNAIMSVIWMITLVLVYKRCYKVIHAMIISLLLPFFSFI 180
 Db 121 DTEVGRALHSILNAIMSVIWMITLVLVYKRCYKVIHAMIISLLLPFFSFI 180
 QY 181 YLGEVFTYVAVDYITVALLINFGVGMISIHMKGPLLQQAIVIMISALMALVFIKY 240
 Db 181 YLGEVFTYVAVDYITVALLINFGVGMISIHMKGPLLQQAIVIMISALMALVFIKY 240
 QY 241 LPEWTAMLIAVISVYDLVAVLCLKGPLRLVETAORNTLTPALISSTWMLVNMAL 300
 Db 241 LPEWTAMLIAVISVYDLVAVLCLKGPLRLVETAORNTLTPALISSTWMLVNMAL 300
 QY 301 GDPRAQRVSKNSKYNASTERSQDTVAENDOGGSEWEAQRDHLGPHRSTPSRAA 360
 Db 301 GDPRAQRVSKNSKYNASTERSQDTVAENDOGGSEWEAQRDHLGPHRSTPSRAA 360
 QY 361 VOELSSITLAGEDEEENGVLGLGDFIFYSVLVGKASATASGMNTTICFVALILGLCL 420
 Db 361 VOELSSITLAGEDEEENGVLGLGDFIFYSVLVGKASATASGMNTTICFVALILGLCL 420
 QY 421 TLLLLAFKKALPALPISITFGLVFPATDYLVQPMDOIAFHQFYI 467
 Db 421 TLLLLAFKKALPALPISITFGLVFPATDYLVQPMDOIAFHQFYI 467

RESULT 5

AAW23964
 ID AAW23964 standard; protein: 467 AA.

XX AAW23964;
 AC
 XX 20-JUL-1998 (first entry)
 DT XX
 DB Human preeslin-1.
 XX
 XX Presentin-1; psi gene; human; familial Alzheimer's disease; PAD;
 KW cerebral haemorrhage; schizophrenia; depression; epilepsy;
 KW mental retardation; diagnosis; therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 26..29 /note= "residue 26-29 deletion, resulting from
 FT alternative splicing"
 FT Misc-difference 79 /note= "Ala73Xaa mutation site"
 FT Domain 82..100 /label= TM1
 FT /note= "transmembrane domain 1"
 FT Misc-difference 82 /note= "Val82Leu mutation site"
 FT Misc-difference 96

FT Domain /note= "Val16Phe mutation site"
 FT 101..132 /label= TM1-2
 FT /note= "hydrophilic loop"
 FT Misc-difference 115 /note= "Tyr115His mutation site"
 FT 133..154 /label= TM2
 FT /note= "transmembrane domain 2"
 FT Misc-difference 139 /note= "Met139Val mutation site"
 FT 139 /note= "Met139Val mutation site"
 FT Misc-difference 139 /note= "Met139Thr mutation site"
 FT 143 /note= "Met139Thr mutation site"
 FT Misc-difference 143 /note= "Ile143Thr mutation site (Claim 18)"
 FT 146 /note= "Met146Val mutation site"
 FT Misc-difference 146 /note= "Met146Leu mutation site (Claim 18)"
 FT 155..163 /label= TM2-3
 FT /note= "hydrophilic loop"
 FT Misc-difference 163 /note= "His163Tyr mutation site"
 FT 163 /note= "His163Arg mutation site"
 FT Domain 164..183 /label= TM3
 FT /note= "transmembrane domain 3"
 FT Misc-difference 171 /note= "Leu171Pro mutation site (Claim 18)"
 FT 177 /note= "Phe117Ser mutation site (Claim 1)"
 FT Domain 184..194 /label= TM3-4
 FT /note= "hydrophilic loop"
 FT 195..212 /label= TM4
 FT /note= "transmembrane domain 4"
 FT Misc-difference 209 /note= "Gly209Val mutation site"
 FT 211 /note= "Ile211Thr mutation site"
 FT Domain 213..220 /label= TM4-5
 FT /note= "hydrophilic loop"
 FT 221..238 /label= TM5
 FT /note= "transmembrane domain 5"
 FT Misc-difference 231 /note= "Ala231Thr mutation site"
 FT 239..243 /label= TM5-6
 FT /note= "hydrophilic loop"
 FT 244..262 /label= TM6
 FT /note= "transmembrane domain 6"
 FT Misc-difference 246 /note= "Ala246Glu mutation site"
 FT 257 /note= "Asp257Ala mutation site, associated with residue
 FT 258-290 deletion (Claim 1)"
 FT Misc-difference 258..290 /note= "residue 258-290 deletion mutant, associated with
 FT Asp257Ala mutation (Claim 1)"
 FT 260 /note= "Ala260Val mutation site (Claim 18)"
 FT Domain 263..407 /label= TM6-7
 FT /note= "hydrophilic loop"
 FT Misc-difference 263 /note= "Cys263Arg mutation site (Claim 18)"
 FT Misc-difference 264

FT	Misc-difference	/note= "Pro264Leu mutation site (Claim 18) "	267
FT	Misc-difference	/note= "Pro267Ser mutation site (Claim 18) "	280
FT	Misc-difference	/note= "Glu280Gly mutation site (Claim 18) "	280
FT	Misc-difference	/note= "Glu280Ala mutation site (Claim 18) "	285
FT	Misc-difference	/note= "Ala285Val mutation site (Claim 18) "	286
FT	Misc-difference	/note= "Leu286Val mutation site (Claim 18) "	291, .319
FT	Misc-difference	/note= "residue 291-319 deletion site"	322
FT	Misc-difference	/note= "Leu322Val mutation site (Claim 18) "	384
FT	Misc-difference	/note= "Gly384Ala mutation site"	392
FT	Misc-difference	/note= "Leu392Val mutation site (Claim 18) "	408, .428
FT	Domain	/label= TW8	
FT	Misc-difference	/note= "transmembrane domain 8"	410
FT	Misc-difference	/note= "Cys410Tyr mutation site (Claim 18) "	439
FT	Misc-difference	/note= "Ile439Val mutation site (Claim 1) "	
XX	WO9601549-A2.		
PD	15-JAN-1998.		
XX	04-JUL-1997.	97WO-CA000475.	
XX	05-JUL-1996;	96US-0021673P.	
PR	12-JUL-1996;	96US-0021700P.	
PR	08-NOV-1996;	96US-0029885P.	
PR	02-JAN-1997;	97US-0034580P.	
PA	(TUTOR) UNIV TORONTO GOVERNING COUNCIL.		
PA	(HSCR-) HSC RES & DEV LP.		
PI	St George- Hyslop PH, Fraser PE, Rommens JM;		
PI	WP1; 1998-286355/25.		
DR	N-PSDB; AAV04666.		
XX	New isolated mutant presenilin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening.		
XX	Claim 1; Page 180-182; 238pp; English.		
XX	This polypeptide comprises human presenilin-1 (hPS1). Its amino acid sequence was deduced from an isolated cDNA clone (see AAV04666). Another hps1 sequence (see AAM23965) results from alternative splicing of the hps1 mRNA transcript. A murine PSI homologue (see AAM23966) and a human presenilin-2 protein (see AAM23967) are also provided. Mutations in the PS-1 and PS-2 genes are linked to the development in humans of forms of familial Alzheimer's disease (FAD) and may be causative of other disorders, e.g. cognitive, intellectual, neurological or physiological disorders such as cerebral haemorrhage, schizophrenia, depression, mental retardation and epilepsy. Use of the nucleic acids and proteins comprising or derived from the presenilins is made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Methods for identifying substances that bind to, or modulate the activity of a presenilin protein, and methods for identifying substances that affect the interaction of a presenilin-interacting protein with a presenilin protein are also disclosed		
XX	Sequence 467 AA;		

Query Match
99.5%; Score 2378; DB 2; Length 467;

[illegible]

CC substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139,
 CC 143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269,
 CC 280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding N
 CC -terminals being e.g. A79Y, V82L, A426 and P436S, particularly by
 CC replacing isoleucine of position 213 by another amino-acid especially
 CC threonine. The gene mutant animals e.g. mice can be used as model animals
 CC for the study of human Alzheimer's diseases and to screen and evaluate
 CC substances as candidates for prevention and/or therapy of Alzheimer's
 CC diseases in patients. They can over-produce amyloid beta protein by the
 CC presenilin-1 gene to cause nerve cell death or peeling off in the
 CC hippocampus earlier. Such animals are being pathologically close to human
 CC patients with Alzheimer's diseases. The present sequence represents human
 CC presenilin-1, as given in the present invention
 CC
 XX
 SQ Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNEROEHRDRSLGHEPPLSNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNEROEHRDRSLGHEPPLSNGRPOGNSR 60
 QY 61 QVVEODEDEBELTLKYGAKHVMLEFVPTLQVWVVAATIKSVFYTRKDGQILYTPFTE 120
 DB 61 QVVEODEDEBELTLKYGAKHVMLEFVPTLQVWVVAATIKSVFYTRKDGQILYTPFTE 120
 QY 121 DTEVVGORALHSIINAAMISVIVMTLLVLYKRCYKVIHAMIISILLFFPSFI 180
 DB 121 DTEVVGORALHSIINAAMISVIVMTLLVLYKRCYKVIHAMIISILLFFPSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMHKGPLRLQQAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMHKGPLRLQQAYLIMISALMALVFIKY 240
 QY 241 LPEWTAMLLAVISVYDLVAVLCLKGPLRLMVEAQRNETLFPALYYSTMWLVNMAE 300
 DB 241 LPEWTAMLLAVISVYDLVAVLCLKGPLRLMVEAQRNETLFPALYYSTMWLVNMAE 300
 QY 301 GDPFAQRVSKSKNAESTERESQDTVAENDDGFESEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDPFAQRVSKSKNAESTERESQDTVAENDDGFESEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSIIAGEDEBERGVKLGDFIFYSVLVCKASATASGDMNTTIIACFVALILGLCL 420
 DB 361 VOELSSSIIAGEDEBERGVKLGDFIFYSVLVCKASATASGDMNTTIIACFVALILGLCL 420
 QY 421 TLLLLAIFKCALPALPISITFGLVFPAFDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKCALPALPISITFGLVFPAFDYLVQPFMDQLAFHQFYI 467

RESULT 7
 AAY23897
 ID AAY23897 standard; protein; 467 AA.
 AC AAY23897;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of the wild type human presenilin 1 (PS1) protein.
 XX
 XX Human; presenilin 1; PS1; presenilin-binding protein; interacting domain;
 KW presenilin allele; Alzheimer's disease; senile dementia;
 KW psychiatric disease; schizophrenia; depression; neurological disease;
 KW stroke; cerebral haemorrhage.
 XX
 OS Homo sapiens.
 XX
 XX W09933501-AA.
 XX
 PD 15-JUL-1999.

XX
 PF 06-JAN-1999; 99WO-CA000018.
 XX
 XX 09-JAN-1998; 98US-0070948P.
 XX
 XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 PA
 PI St George- Hyelop PH, Fraser PE;
 DR WPI, 1999-419410/35.
 XX
 PT Identifying substances that alter presenilin interactions, useful for
 PT screening individuals for presenilin alleles associated with Alzheimer's
 PT disease - useful for diagnosis of Alzheimer's disease.
 XX
 PS Disclosure; Page 34-36; 40pp; English.

CC The present sequence represents wild type human presenilin 1 (PS1)
 CC protein. The specification describes a method for identifying substances
 CC that alter the interaction of a presenilin with a presenilin-binding
 CC protein. The method comprises contacting the interacting domain of a
 CC presenilin protein to a presenilin-binding protein in the presence of a
 CC test substance, and measuring the interaction of the presenilin and the
 CC presenilin-binding protein. The method can be used to screen individuals
 CC for presenilin alleles associated with Alzheimer's disease and related
 CC disorders, such as senile dementia's, psychiatric diseases such as
 CC schizophrenia and depression, and neurological disease, such as stroke
 CC and cerebral haemorrhage
 CC
 XX
 SQ Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNEROEHRDRSLGHEPPLSNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNEROEHRDRSLGHEPPLSNGRPOGNSR 60
 QY 61 QVVEODEDEBELTLKYGAKHVMLEFVPTLQVWVVAATIKSVFYTRKDGQILYTPFTE 120
 DB 61 QVVEODEDEBELTLKYGAKHVMLEFVPTLQVWVVAATIKSVFYTRKDGQILYTPFTE 120
 QY 121 DTEVVGORALHSIINAAMISVIVMTLLVLYKRCYKVIHAMIISILLFFPSFI 180
 DB 121 DTEVVGORALHSIINAAMISVIVMTLLVLYKRCYKVIHAMIISILLFFPSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMHKGPLRLQQAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMHKGPLRLQQAYLIMISALMALVFIKY 240
 QY 241 LPEWTAMLLAVISVYDLVAVLCLKGPLRLMVEAQRNETLFPALYYSTMWLVNMAE 300
 DB 241 LPEWTAMLLAVISVYDLVAVLCLKGPLRLMVEAQRNETLFPALYYSTMWLVNMAE 300
 QY 301 GDPFAQRVSKSKNAESTERESQDTVAENDDGFESEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDPFAQRVSKSKNAESTERESQDTVAENDDGFESEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSIIAGEDEBERGVKLGDFIFYSVLVCKASATASGDMNTTIIACFVALILGLCL 420
 DB 361 VOELSSSIIAGEDEBERGVKLGDFIFYSVLVCKASATASGDMNTTIIACFVALILGLCL 420
 QY 421 TLLLLAIFKCALPALPISITFGLVFPAFDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKCALPALPISITFGLVFPAFDYLVQPFMDQLAFHQFYI 467

RESULT 8
 AAB07971
 ID AAB07971 standard; protein; 467 AA.
 AC AAB07971;

XX 14-NOV-2000 (first entry)
 XX Amino acid sequence of human presenilin 1 polypeptide.
 DE Human; presenilin; PS1; PS2; nerve cell growth; nerve damage; hNRPAP;
 XX Human; plakophilin related armidillo protein; Alzheimer's disease;
 KM Parkinson's disease; amyotrophic lateral sclerosis; ALS; stroke;
 KM multiple sclerosis; ischemia; stroke; neural paropathy; sciatic crush;
 KM motor neuron disease; peripheral neuropathy; neuropathy; diabetes;
 KM spinal cord injury; facial nerve crush.
 XX Homo sapiens.
 OS WO200047615-A2.
 XX 17-AUG-2000.
 PD 11-FEB-2000; 2000WO-CA000126.
 XX 12-FEB-1999; 99US-0119835P.
 XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 PA St George- Hyslop PH, Fraser PE;
 XX PI WPI; 2000-524531/47.
 XX Stimulation of nerve cell growth using human Neural Plakophilin Related
 PT Armidillo Protein (hNRPAP) polypeptide, useful for the treatment of
 PT diseases such as Alzheimer's, Parkinson's, and stroke.
 XX Disclosure; Page 19-20; 33pp; English.
 XX The present sequence represents a human presenilin 1 (PS1) polypeptide.
 CC Human Neural Plakophilin Related Armidillo Protein (hNRPAP) polypeptide.
 CC is known to interact with PS1 and PS2. The specification describes a
 CC method for stimulating the growth of nerve cells, comprising contacting
 CC them with hNRPAP. The hNRPAP polypeptide and polynucleotide are useful
 CC for treating nerve damage caused by a variety of diseases or physical
 CC traumas, including Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis (ALS), multiple sclerosis, stroke, ischemia associated
 CC with stroke, neural paropathy, motor neuron diseases, sciatic crush,
 CC peripheral neuropathy, neuropathy associated with diabetes, spinal cord
 CC injuries and facial nerve crush
 CC Sequence 467 AA;
 SQ

Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFONAMQSEDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60
 DB 1 MTELPAPLSTYFONAMQSEDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60
 QY 61 QVVEDEDEDEDELTKYAKAVIMLFVPVTLQMVVAVATISVSFYYRKQGLLYTPTFE 120
 DB 61 QVVEDEDEDEDELTKYAKAVIMLFVPVTLQMVVAVATISVSFYYRKQGLLYTPTFE 120
 QY 121 DTEIVGQALSHLSILMAIMISIVVMWILLVLYKRCYKIHMLTISSLLFFPSFI 180
 DB 121 DTEIVGQALSHLSILMAIMISIVVMWILLVLYKRCYKIHMLTISSLLFFPSFI 180
 QY 121 DTEIVGQALSHLSILMAIMISIVVMWILLVLYKRCYKIHMLTISSLLFFPSFI 180
 DB 121 DTEIVGQALSHLSILMAIMISIVVMWILLVLYKRCYKIHMLTISSLLFFPSFI 180
 QY 181 YLGEVFKTYNVAVDITVALLIMNGVGMISIMKGLRLQOAYLIMISLMLVPIKY 240
 DB 181 YLGEVFKTYNVAVDITVALLIMNGVGMISIMKGLRLQOAYLIMISLMLVPIKY 240
 QY 241 LPENTAMILLAVISYVDLVAVALCKGPKRLMVEAQENETLFPALITYSSIMVLMVAE 300
 DB 241 LPENTAMILLAVISYVDLVAVALCKGPKRLMVEAQENETLFPALITYSSIMVLMVAE 300
 QY 301 GDPKQKRVSKSKNAESTERESODIVAENDDGGFSEMEPAQRDSHLGHPRSTPESRAA 360
 DB 301 GDPKQKRVSKSKNAESTERESODIVAENDDGGFSEMEPAQRDSHLGHPRSTPESRAA 360

DB 301 GDPKQKRVSKSKNAESTERESODIVAENDDGGFSEMEPAQRDSHLGHPRSTPESRAA 360
 QY 361 VOELSSSIIAGDEPBERGVAGLGDFFYSVLVGRXSATASGMWNTTICFVAILGLCL 420
 DB 361 VOELSSSIIAGDEPBERGVAGLGDFFYSVLVGRXSATASGMWNTTICFVAILGLCL 420
 QY 421 TLLLLAFKKALPALPISITFGLVFFYFATDYLVQPFMDQLAFQFYI 467
 DB 421 TLLLLAFKKALPALPISITFGLVFFYFATDYLVQPFMDQLAFQFYI 467

RESULT 9
 AAE10798
 ID AAE10798 standard; protein; 467 AA.
 XX AAE10798;
 AC 18-DEC-2001 (first entry)
 DT Human presenilin-1 (PS-1) protein.
 XX Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy;
 KM neurodegenerative disease; Alzheimer's disease; noctropic; prophylaxis;
 KM neuronal disorder; cognitive disorder.
 XX Homo sapiens.
 OS WO200167097-A2.
 XX 13-SEP-2001.
 PD 09-MAR-2001; 2001WO-GB001059.
 XX 10-MAR-2000; 2000GB-00005895.
 XX (GLAX) GLAXO GROUP LTD.
 XX Hale RS, Rowley A, Blackstock W;
 XX WPI; 2001-589954/66.
 DR N-PSDB; AAD18120.
 XX Identifying presenilin or catenin p120 activity modulator useful for
 PT modulating presenilin-catenin p120 interaction and thus for treating
 PT cognitive disorder e.g., Alzheimer's disease comprises enhancing
 PT cognitive function.
 XX Example 1; Page 41-42; 48pp; English.
 PS The invention relates to a method for identifying modulators of
 XX presenilin and catenin p120. Modulators of catenin p120 and presenilin
 CC are useful for the treatment and prophylaxis of disorders that is
 CC responsive to modulation of presenilin/catenin p120 activity. In
 CC particular, neuronal disorders such as cognitive disorders and
 CC neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNAs
 CC are useful for identifying mutations in catenin p120 genes.
 CC Identification of such mutations assist in the diagnosis of or
 CC susceptibility to Alzheimer's or other conditions associated with
 CC presenilin and in assessing the physiology of such disorders. Catenin
 CC p120 DNAs are also used in hybridisation studies to monitor expression of
 CC p120 genes and in particular for up or down regulation of catenin p120
 CC expression. The present sequence is human presenilin-1 (PS-1) protein
 CC Sequence 467 AA;
 SQ

Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFONAMQSEDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60
 DB 1 MTELPAPLSTYFONAMQSEDNHLSNTVRSQNDNRROEHNDRLSGHPEPLSNGRPOGNSR 60

CC the treatment or prophylaxis of Alzheimer's disease. The KIAA0253
 CC polynucleotide and KIAA0253 polypeptide are useful in the treatment,
 CC prophylaxis or diagnosis of Alzheimer's disease

XX
 SQ Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSR 60
 DB 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSR 60
 QY 61 QVVEDEDEBELTLKYGAKVIMLFVPTLCMVAATIKSVSFYTRKDGQILYTPFTE 120
 DB 61 QVVEDEDEBELTLKYGAKVIMLFVPTLCMVAATIKSVSFYTRKDGQILYTPFTE 120
 QY 121 DTEVGGQALHSINAAIMISVIVMTLLVLYKYRCYKVIHMLIISLLLPFSFI 180
 DB 121 DTEVGGQALHSINAAIMISVIVMTLLVLYKYRCYKVIHMLIISLLLPFSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISHWKGLRQQAYLIMISALMLVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISHWKGLRQQAYLIMISALMLVFIKY 240
 QY 241 LPEWTAMTILAVISYVDLVAVLCLKGRLMLETQERNETLFPALIISSSTMWLVNMAE 300
 DB 241 LPEWTAMTILAVISYVDLVAVLCLKGRLMLETQERNETLFPALIISSSTMWLVNMAE 300
 QY 301 GDPKQRRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 DB 301 GDPKQRRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 QY 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFVAIILIGLCL 420
 DB 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467

RESULT 10
 AAG63936
 ID AAG63936 standard; protein; 467 AA.
 AC AAG63936;
 DT 29-OCT-2001 (first entry)
 DE Amino acid sequence of human presenilin 1.
 KW KIAA0253; presenilin; Alzheimer's disease.
 OS Homo sapiens.
 PN WO200167109-A1.
 PD 13-SEP-2001.
 PF 09-MAR-2001; 2001WO-GB001057.
 PR 10-MAR-2000; 2000GB-00005894.
 PA (GLAXO) GLAXO GROUP LTD.
 PI Hale RS, Rowley A, Blackstock W;
 DR WPI; 2001-522960/57.
 DR N-PSDB; AAH74993.
 PT Identifying a modulator of presenilin function by determining the ability
 of presenilin to bind to a KIAA0253 polypeptide in the presence and
 absence of a test compound, useful in the treatment or prophylaxis of
 Alzheimer's disease.
 PS Disclosure; Page 40-41; 48pp; English.
 CC The present sequence represents human presenilin 1. KIAA0253 binds to
 CC presenilin. The specification describes a method of identifying a
 CC modulator of presenilin function or KIAA0253 function. The method
 CC comprises determining presenilin activity or KIAA0253 activity in the
 CC presence and absence of a test compound, where presenilin activity is
 CC determined by its ability to bind to KIAA0253. A modulator of presenilin
 CC or KIAA0253 polypeptide is useful in the manufacture of a medicament for

CC the treatment or prophylaxis of Alzheimer's disease. The KIAA0253
 CC polynucleotide and KIAA0253 polypeptide are useful in the treatment,
 CC prophylaxis or diagnosis of Alzheimer's disease

XX
 SQ Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSR 60
 DB 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSR 60
 QY 61 QVVEDEDEBELTLKYGAKVIMLFVPTLCMVAATIKSVSFYTRKDGQILYTPFTE 120
 DB 61 QVVEDEDEBELTLKYGAKVIMLFVPTLCMVAATIKSVSFYTRKDGQILYTPFTE 120
 QY 121 DTEVGGQALHSINAAIMISVIVMTLLVLYKYRCYKVIHMLIISLLLPFSFI 180
 DB 121 DTEVGGQALHSINAAIMISVIVMTLLVLYKYRCYKVIHMLIISLLLPFSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISHWKGLRQQAYLIMISALMLVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISHWKGLRQQAYLIMISALMLVFIKY 240
 QY 241 LPEWTAMTILAVISYVDLVAVLCLKGRLMLETQERNETLFPALIISSSTMWLVNMAE 300
 DB 241 LPEWTAMTILAVISYVDLVAVLCLKGRLMLETQERNETLFPALIISSSTMWLVNMAE 300
 QY 301 GDPKQRRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 DB 301 GDPKQRRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 QY 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFVAIILIGLCL 420
 DB 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDWNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467

RESULT 11
 AAE05466
 ID AAE05466 standard; protein; 467 AA.
 AC AAE05466;
 DT 24-SEP-2001 (first entry)
 DE Human presenilin (Psi) protein.
 KW Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
 KW NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
 KW peripheral neuropathy; motor neuron disorder; neurodegenerative disorder;
 KW Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
 KW Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
 KW nerve deafness; Alzheimer's disease; epilepsy.
 OS Homo sapiens.
 PN WO200151671-A2.
 PD 19-JUL-2001.
 PF 08-JAN-2001; 2001WO-US000526.
 PR 10-JAN-2000; 2000US-0175200P.
 PR 04-JAN-2001; 2001US-00754949.
 PA (SCIO-) SCIOS INC.
 CC

QY 241 LPEWTAMLLAVISYVDVAVLCKGPIRLMVEIAOERNETLFPALIVYSTWVLYNMAE 300
 DB 241 LPEWTAMLLAVISYVDVAVLCKGPIRLMVEIAOERNETLFPALIVYSTWVLYNMAE 300
 QY 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALILGCL 420
 DB 361 VOELSSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALILGCL 420
 QY 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOFPMDQLAFHOXYI 467
 DB 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOFPMDQLAFHOXYI 467

RESULT 13
 AAU79416
 ID AAU79416 standard; protein; 467 AA.
 AC AAU79416;
 DT 02-SEP-2002 (first entry)
 DE Human presentin-1, PS-1.
 KW Human; integrin-linked kinase; ILK; presentin-1; protein kinase B; PKB;
 KM gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;
 OS neoprotective; cytosolic; cancer.
 XX Homo sapiens.
 XX MO20022862-A2.
 XX 21-MAR-2002.
 XX 12-SEP-2001; 2001WO-GB004094.
 XX 12-SEP-2000; 2000GB-00022333.
 XX (GLAX) GLAXO GROUP LTD.
 XX Hiles ID, Ellis C;
 XX WPI; 2002-351896/38.

Identifying agent that modulates interaction between integrin-linked kinase and presentin-1, useful for treating Alzheimer's disease, and identifying agent that modulates protein kinase B or gamma secretase activity.

Disclosure; Page 43-45; 53pp; English.

The invention relates to identifying an agent modulating interaction between integrin-linked kinase (ILK) and presentin-1 (PS1) comprising providing ILK, PSI or their functional variants, as first and second components respectively, contacting the components in the presence of a test agent under conditions that in absence of the agent, would permit the components to interact and determining whether the agent is capable of modulating the interaction between the components. Also included are the method above where the components are protein kinase beta (PKB), gamma secretase or their functional variants, test kits for carrying out the methods and an agent identified by the methods. The methods are used for identifying an agent that modulates interaction between ILK and PSI, or PKB or gamma-secretase. The agent has therapeutic applications in treating humans or animals, for treating a host suffering from a condition associated with an interaction between ILK and PSI, activity of PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's disease. The agent is also useful for manufacturing a medicament for use in treatment of the above mentioned conditions. The present sequence represents human presentin-1, PS-1

SQ Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 5; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1,4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPISYQNAQMSQEDNLSNTVRSQNDNRROEHNDRLSGHPPLSNRPOQNSR 60
 DB 1 MTELPAPISYQNAQMSQEDNLSNTVRSQNDNRROEHNDRLSGHPPLSNRPOQNSR 60
 QY 61 QVBODEDEDEELTKGAKAVIMLFVPTLCMVVVAATIKSVSFYTRKQGLITYPTE 120
 DB 61 QVBODEDEDEELTKGAKAVIMLFVPTLCMVVVAATIKSVSFYTRKQGLITYPTE 120
 QY 121 DTEIVGQALSHSIINAAIMISIVVMTLLVLYKRCYKITHWLLISLLLPFSFI 180
 DB 121 DTEIVGQALSHSIINAAIMISIVVMTLLVLYKRCYKITHWLLISLLLPFSFI 180
 QY 181 YLGEVFKTYNNAVDYITVALLIMNGVYGMISHHKGPLRQOAYLIMISALMLVFIFY 240
 DB 181 YLGEVFKTYNNAVDYITVALLIMNGVYGMISHHKGPLRQOAYLIMISALMLVFIFY 240
 QY 241 LPEWTAMLLAVISYVDVAVLCKGPIRLMVEIAOERNETLFPALIVYSTWVLYNMAE 300
 DB 241 LPEWTAMLLAVISYVDVAVLCKGPIRLMVEIAOERNETLFPALIVYSTWVLYNMAE 300
 QY 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALILGCL 420
 DB 361 VOELSSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALILGCL 420
 QY 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOFPMDQLAFHOXYI 467
 DB 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOFPMDQLAFHOXYI 467

RESULT 14
 AA018049
 ID AA018049 standard; protein; 467 AA.
 AC AA018049;
 DT 02-SEP-2002 (first entry)
 DE Presentin protein.
 KW Sel-12; presentin; neuronal disorder; familial Alzheimer's disease; amyloid precursor protein; APP.
 XX Unidentified.
 XX US6376239-B1.
 XX 23-APR-2002.
 XX 04-APR-1997; 97US-00832867.
 XX 04-APR-1997; 97US-00832867.
 XX (ELBG-) ELBGENE GMBH.
 XX Baumeister R;
 XX WPI; 2002-478281/51.
 XX N-PSDB; AAL47323.

Isolated DNA molecule comprising promoter of the sel-12 gene from Caenorhabditis elegans operably linked to heterologous gene, directs expression in neural cells and is useful to develop drugs to treat neuronal disorders.

XX Claim 2; Fig 4; 78p; English.
 XX
 CC The present invention relates to DNA molecules comprising the promoter of
 CC the sel-12 gene from *Caenorhabditis elegans* operably linked to a
 CC heterologous DNA sequence encoding a protein of interest. The sequence
 CC can be used to develop drugs for the treatment, prevention or delay of a
 CC neuronal disorder. In particular, the neuronal disorder may be familial
 CC Alzheimer's disease. The present sequence is a presentin protein
 CC described in the exemplification of the invention

XX Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 5; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQENDRSLGHPPLNSGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQENDRSLGHPPLNSGRPGNSR 60
 QY 61 QVVEODEEDELTLTKYGAHVIMLFPVPTLCMVVVAATIKSVSPYTRDQGLITPPT 120
 DB 61 QVVEODEEDELTLTKYGAHVIMLFPVPTLCMVVVAATIKSVSPYTRDQGLITPPT 120
 QY 121 DRETGQRALHSILNAAIMISIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
 DB 121 DRETGQRALHSILNAAIMISIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
 QY 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPRLQOAYLIMSALMLVFIKY 240
 DB 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPRLQOAYLIMSALMLVFIKY 240
 QY 241 LPEMTAMLIATISYVDLVAVLCCKPPLMLVETAOERNETLFPALISSTWMLVNMAB 300
 DB 241 LPEMTAMLIATISYVDLVAVLCCKPPLMLVETAOERNETLFPALISSTWMLVNMAB 300
 QY 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEMEARQDSHLGPHRSTPESRA 360
 DB 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEMEARQDSHLGPHRSTPESRA 360
 QY 361 VOELSSSIIAGDEPBERGVKLGDFIFYSVVGKASATASGDMNTTIACFAVAILIGL 420
 DB 361 VOELSSSIIAGDEPBERGVKLGDFIFYSVVGKASATASGDMNTTIACFAVAILIGL 420
 QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHOFYI 467
 DB 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHOFYI 467

RESULT 15

AA05737
 ID AAM05737 standard; protein; 467 AA.

XX AC AAM05737;

XX DT 25-MAR-2003 (revised)
 DT 23-JUL-1997 (first entry)

XX DE Presentin-1-1 V82L mutation.

XX KW Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrētia;
 KW depression; antibody; gene expression modulator; therapy; mutuin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Modified-site 82
 FT /label= V82L

XX WO9634099-A2.

PD 31-OCT-1996.
 XX
 XX PF 29-APR-1996; 96MO-CA000263.
 XX
 PR 28-APR-1995; 95US-00431048.
 PR 28-JUN-1995; 95US-00496841.
 PR 31-JUL-1995; 95US-00509359.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 XX
 PI St George's Hospital PH, Fraser PE, Rommens JM;
 DR WPI; 1996-497631/49.
 XX
 PT New presentin genes - useful for diagnosis, therapy and drug screening
 PT of familial Alzheimer's disease, cerebral disorders, etc.
 PS
 PS Claim 3; Page; 178pp; English.

CC AAM05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot spot
 CC regions. Mutations in PS genes are implicated in familial Alzheimer's
 CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
 CC schizophrenia, depression etc., so detection of mutations in the DNA
 CC encoding the wild type sequences can be used for diagnosis of these
 CC diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are useful
 CC as models for drug screening. The antibodies can also be used e.g. for
 CC affinity purification and in immunoassays. (updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 XX
 SQ Sequence 467 AA;

Query Match 99.3%; Score 2375; DB 2; Length 467;
 Best Local Similarity 99.4%; Pred. No. 2.8e-233;
 Matches 464; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQENDRSLGHPPLNSGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQENDRSLGHPPLNSGRPGNSR 60
 QY 61 QVVEODEEDELTLTKYGAHVIMLFPVPTLCMVVVAATIKSVSPYTRDQGLITPPT 120
 DB 61 QVVEODEEDELTLTKYGAHVIMLFPVPTLCMVVVAATIKSVSPYTRDQGLITPPT 120
 QY 121 DRETGQRALHSILNAAIMISIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
 DB 121 DRETGQRALHSILNAAIMISIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
 QY 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPRLQOAYLIMSALMLVFIKY 240
 DB 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPRLQOAYLIMSALMLVFIKY 240
 QY 241 LPEMTAMLIATISYVDLVAVLCCKPPLMLVETAOERNETLFPALISSTWMLVNMAB 300
 DB 241 LPEMTAMLIATISYVDLVAVLCCKPPLMLVETAOERNETLFPALISSTWMLVNMAB 300
 QY 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEMEARQDSHLGPHRSTPESRA 360
 DB 301 GDEPAQRVSKSKNAESTERESODTVAENDDGFSEMEARQDSHLGPHRSTPESRA 360
 QY 361 VOELSSSIIAGDEPBERGVKLGDFIFYSVVGKASATASGDMNTTIACFAVAILIGL 420
 DB 361 VOELSSSIIAGDEPBERGVKLGDFIFYSVVGKASATASGDMNTTIACFAVAILIGL 420
 QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHOFYI 467

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Page 12

Db 421 TTTTTTIFKKALPALPISITFGLVFFATDYLWQPMQALAFHQFYI 467

Search completed: April 8, 2004, 16:56:31
Job time : 62 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:58:26 ; Search time 47 Seconds

(without alignments)
2612.596 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391
Sequence: 1 MTELRAPUSYFONAGMSEDN.....ATDVLVQPMQALFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2384	99.7	467	9	US-09-785-474-2
3	2379	99.5	467	9	US-09-785-474-32
4	2378	99.5	467	9	US-09-754-949-4
5	2378	99.5	467	9	US-09-878-454A-3
6	2378	99.5	467	9	US-09-895-035-14
7	2378	99.5	467	13	US-10-071-900-1
8	2378	99.5	467	14	US-10-221-254-4
9	2378	99.5	467	15	US-10-417-422-4
10	2374	99.3	467	9	US-09-785-474-4
11	2372	99.2	467	9	US-09-785-474-28
12	2348	98.2	463	9	US-09-895-035-12
13	2266	94.8	467	14	US-10-293-000-5
15	1452	60.7	448	9	US-09-878-454A-1

16	1452	60.7	448	13	US-10-071-900-2	Sequence 2, Appli
17	1452	60.7	448	14	US-10-293-000-6	Sequence 6, Appli
18	1452	60.7	448	14	US-10-180-781-2	Sequence 2, Appli
19	1444	60.4	448	9	US-09-754-949-6	Sequence 6, Appli
20	1444	60.4	448	14	US-10-221-254-6	Sequence 6, Appli
21	1444	60.4	448	15	US-10-417-422-6	Sequence 1, Appli
22	798.5	33.4	180	9	US-09-895-035-1	Sequence 8, Appli
23	653	27.3	354	9	US-09-823-153-8	Sequence 6, Appli
24	552.5	23.1	478	12	US-10-425-11-60796	Sequence 47501, A
25	552.5	23.1	481	12	US-10-425-11-47501	Sequence 30637, A
26	377	15.8	80	14	US-10-029-386-30637	Sequence 1227, Ap
27	365	15.3	101	9	US-09-925-299-1227	Sequence 1227, Ap
28	365	15.3	101	10	US-09-925-299-1227	Sequence 11, Appl
29	362.5	15.2	129	14	US-10-051-767-11	Sequence 12, Appl
30	361.5	15.1	111	14	US-10-051-767-10	Sequence 12, Appl
31	335	14.0	210	12	US-10-051-767-12	Sequence 12, Appl
32	328.5	13.7	233	12	US-10-424-539-196951	Sequence 196951, A
33	299	12.5	166	14	US-10-051-767-7	Sequence 7, Appl
34	299	12.5	166	14	US-10-051-767-13	Sequence 13, Appl
35	278.5	11.6	177	12	US-10-424-599-196783	Sequence 196783, A
36	246	10.3	74	14	US-10-051-767-9	Sequence 9, Appli
37	246	10.3	74	14	US-10-051-767-15	Sequence 15, Appl
38	243.5	10.2	65	9	US-09-864-761-38056	Sequence 38056, A
39	235.5	9.8	124	15	US-10-411-207-6	Sequence 6, Appli
40	231.5	9.7	98	12	US-10-424-599-209024	Sequence 209024, A
41	221	9.2	60	12	US-10-424-599-203174	Sequence 203174, A
42	198	8.3	42	14	US-10-029-386-28604	Sequence 28604, A
43	194	8.1	124	14	US-10-051-767-8	Sequence 8, Appli
44	194	8.1	124	14	US-10-051-767-14	Sequence 14, Appl
45	120.5	5.0	2386	15	US-10-369-493-2379	Sequence 2379, Ap

ALIGNMENTS

RESULT 1
US-09-785-474-30
Sequence 30, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
MASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
NUMBER OF SEQUENCES: 32
ADDRESSSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
 US-09-785-474-30

Query Match 100.0%; Score 2391; DB 9; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1,5e-206;

Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPPLSGRPOGNSR 60
QY 61 QVEODEEEDDELTLTKGAKHIVMLFVPTLCMVVVAATIKSVSFYTRDGLIYTPFTE 120
DB 61 QVEODEEEDDELTLTKGAKHIVMLFVPTLCMVVVAATIKSVSFYTRDGLIYTPFTE 120
QY 121 DTEYQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLFFFSFI 180
DB 121 DTEYQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLFFFSFI 180
QY 121 DTEYQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLFFFSFI 180
DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
QY 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
QY 241 LPENWAMTLIAVISYDVAVALCKGPLRLMVELTQERNETLFPALISSIVMWLVNMAE 300
DB 241 LPENWAMTLIAVISYDVAVALCKGPLRLMVELTQERNETLFPALISSIVMWLVNMAE 300
QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEBWEAQRDHLGPHRSTPESRAA 360
DB 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEBWEAQRDHLGPHRSTPESRAA 360
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DB 361 VOELSSSIIAGDPEERGVKLGDPFIYSVLVGRASATASGDWNTTIACFVALILIGLCL 420
QY 361 VOELSSSIIAGDPEERGVKLGDPFIYSVLVGRASATASGDWNTTIACFVALILIGLCL 420
DB 361 VOELSSSIIAGDPEERGVKLGDPFIYSVLVGRASATASGDWNTTIACFVALILIGLCL 420
QY 421 TLILLAIFFKALPALPISITFGLVFATDYLVOPFMDOLAFHOFYI 467
DB 421 TLILLAIFFKALPALPISITFGLVFATDYLVOPFMDOLAFHOFYI 467

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RESULT 2

US-09-785-474-2
 Sequence 2, Application US/09785474
 Patent No. US20010012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH
 MASCO, WILLMA

TITLE OF INVENTION: Genetic Alterations Related To Familial
 Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

APPLICATION NUMBER: US/09/785,474
 FILING DATE: 20-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,344

FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/003,054
 FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-785-474-2

Query Match 99.7%; Score 2384; DB 9; Length 467;
 Best Local Similarity 99.8%; Pred. No. 6,2e-206;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 QVEODEEEDDELTLTKGAKHIVMLFVPTLCMVVVAATIKSVSFYTRDGLIYTPFTE 120
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QY 121 DTEYQGRALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLFFFSFI 180
DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
QY 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
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DB 241 LPENWAMTLIAVISYDVAVALCKGPLRLMVELTQERNETLFPALISSIVMWLVNMAE 300
QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEBWEAQRDHLGPHRSTPESRAA 360
DB 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEBWEAQRDHLGPHRSTPESRAA 360
QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEBWEAQRDHLGPHRSTPESRAA 360
DB 361 VOELSSSIIAGDPEERGVKLGDPFIYSVLVGRASATASGDWNTTIACFVALILIGLCL 420
QY 361 VOELSSSIIAGDPEERGVKLGDPFIYSVLVGRASATASGDWNTTIACFVALILIGLCL 420
DB 361 VOELSSSIIAGDPEERGVKLGDPFIYSVLVGRASATASGDWNTTIACFVALILIGLCL 420
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DB 421 TLILLAIFFKALPALPISITFGLVFATDYLVOPFMDOLAFHOFYI 467

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RESULT 3

US-09-785-474-32
 Sequence 32, Application US/09785474
 Patent No. US20010012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH
 MASCO, WILLMA

TITLE OF INVENTION: Genetic Alterations Related To Familial
 Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/785,474
 FILING DATE: 20-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/706,344
 FILING DATE: 30-AUG-1996
 APPLICATION NUMBER: 60/003,054
 FILING DATE: 31-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: KIM, JUDITH U.
 REGISTRATION NUMBER: 40,679
 REFERENCE/DOCKET NUMBER: 0609,4180002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-09-785-474-32

Query Match 99.5%; Score 2379; DB 9; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1,7e-205;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MTELPAPLSYFQNAQWSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNGRPOGNSR 60
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QY 121 DTEVGOQALHSILNAIMISVIYVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
DB 121 DTEVGOQALHSILNAIMISVIYVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
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DB 181 YLGEVFKTYNAVVDITVALLIMNFGVGMISIMHKGPRLQOAYLIMISALMAVFIKY 240
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DB 241 LPEWTAMLLAVISYVDLVAVLCLKGPLRMLVETAQERNETLFPALISSTWMLVNMAL 300
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DB 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMMTTIACFAVAILIGLCL 420
DB 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMMTTIACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467

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RESULT 4
 US-09-754-949-4
 Sequence 4, Application US/09754949
 Patent No. US20020015939A1
 GENERAL INFORMATION:

APPLICANT: MCCARTHY, JUSTIN
 APPLICANT: CORDELL, BARBARA
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
 TITLE OF INVENTION: NEURONAL DEGENERATION
 FILE REFERENCE: SCIOS.012A
 CURRENT APPLICATION NUMBER: US/09/754,949
 CURRENT FILING DATE: 2001-01-04
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-754-949-4

Query Match 99.5%; Score 2378; DB 9; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2,2e-205;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MTELPAPLSYFQNAQWSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNGRPOGNSR 60
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DB 61 QVVEODEEDELTLKYGAKHYIMLFVPTLCMVVVVAITIKSVSFYTRKQGLITPTE 120
QY 121 DTEVGOQALHSILNAIMISVIYVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
DB 121 DTEVGOQALHSILNAIMISVIYVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNAVVDITVALLIMNFGVGMISIMHKGPRLQOAYLIMISALMAVFIKY 240
DB 181 YLGEVFKTYNAVVDITVALLIMNFGVGMISIMHKGPRLQOAYLIMISALMAVFIKY 240
QY 241 LPEWTAMLLAVISYVDLVAVLCLKGPLRMLVETAQERNETLFPALISSTWMLVNMAL 300
DB 241 LPEWTAMLLAVISYVDLVAVLCLKGPLRMLVETAQERNETLFPALISSTWMLVNMAL 300
QY 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
DB 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMMTTIACFAVAILIGLCL 420
DB 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMMTTIACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFPATDYLVPFMDQLAFHOFYI 467

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RESULT 5
 US-09-878-454A-3
 Sequence 3, Application US/09878454A
 Patent No. US20020064828A1
 GENERAL INFORMATION:
 APPLICANT: Monteliro, et al.
 TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentlin
 FILE REFERENCE: 4115-161
 CURRENT APPLICATION NUMBER: US/09/878,454A
 CURRENT FILING DATE: 2001-06-11
 PRIOR APPLICATION NUMBER: 60/210,939
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 3
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-878-454A-3

Query Match 99.5%; Score 2378; DB 9; Length 467;

Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQENHNRSLGHPZPLSNGRPQNSR 60
QY 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQILITPTE 120
Db 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQILITPTE 120
QY 121 DTEVGOALHSLINAAIMSVIWMITLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db 121 DTEVGOALHSLINAAIMSVIWMITLLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMALVFICY 240
Db 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMALVFICY 240
QY 241 LPEWTAMLIIVSVYDLVAVLCLKGRLMVLTAQERNETLFPALISSTWMLVNMAB 300
Db 241 LPEWTAMLIIVSVYDLVAVLCLKGRLMVLTAQERNETLFPALISSTWMLVNMAB 300
QY 301 GDEPAQRVSKNSKNAESTERESQDTVAENDGGESEWEAQRDHLGPHRSTPESRAA 360
Db 301 GDEPAQRVSKNSKNAESTERESQDTVAENDGGESEWEAQRDHLGPHRSTPESRAA 360
QY 361 VOELSSILAGEPBERGVKLGDFIFSVLVGKASATSGDMNTTACFAVAILIGLCL 420
Db 361 VOELSSILAGEPBERGVKLGDFIFSVLVGKASATSGDMNTTACFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVIFYFATDYLQPFMDQLAFHQFYI 467
Db 421 TLLLLAIFKKALPALPISITFGVIFYFATDYLQPFMDQLAFHQFYI 467

RESULT 6
US-09-895-035-14
Sequence 14, Application US/09895035
Patent No. US2002008211A1
GENERAL INFORMATION:
APPLICANT: Patterson, Chandra
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN PRESENTILIN VARIANT
FILE REFERENCE: PC-0047 CIP
CURRENT APPLICATION NUMBER: US/09/895, 035
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/116, 640
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2002008211A1 g1709856
US-09-895-035-14

Query Match 99.5%; Score 2378; DB 9; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQENHNRSLGHPZPLSNGRPQNSR 60
Db 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQENHNRSLGHPZPLSNGRPQNSR 60
QY 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQILITPTE 120
Db 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQILITPTE 120

QY 121 DTEVGOALHSLINAAIMSVIWMITLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db 121 DTEVGOALHSLINAAIMSVIWMITLLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMALVFICY 240
Db 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMALVFICY 240
QY 241 LPEWTAMLIIVSVYDLVAVLCLKGRLMVLTAQERNETLFPALISSTWMLVNMAB 300
Db 241 LPEWTAMLIIVSVYDLVAVLCLKGRLMVLTAQERNETLFPALISSTWMLVNMAB 300
QY 301 GDEPAQRVSKNSKNAESTERESQDTVAENDGGESEWEAQRDHLGPHRSTPESRAA 360
Db 301 GDEPAQRVSKNSKNAESTERESQDTVAENDGGESEWEAQRDHLGPHRSTPESRAA 360
QY 361 VOELSSILAGEPBERGVKLGDFIFSVLVGKASATSGDMNTTACFAVAILIGLCL 420
Db 361 VOELSSILAGEPBERGVKLGDFIFSVLVGKASATSGDMNTTACFAVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVIFYFATDYLQPFMDQLAFHQFYI 467
Db 421 TLLLLAIFKKALPALPISITFGVIFYFATDYLQPFMDQLAFHQFYI 467

RESULT 7
US-10-071-900-1
Sequence 1, Application US/10071900
Publication No. US20020127541A1
GENERAL INFORMATION:
APPLICANT: St. George-Hyslop, Peter H.
APPLICANT: Rommens, Joanna
APPLICANT: Fraser, Paul E.
TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
FILE REFERENCE: 1034/1F810-US1
CURRENT APPLICATION NUMBER: US/10/071, 900
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/227, 725
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 467
TYPE: PRT
ORGANISM: Homo Sapien
US-10-071-900-1

Query Match 99.5%; Score 2378; DB 13; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQENHNRSLGHPZPLSNGRPQNSR 60
Db 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQENHNRSLGHPZPLSNGRPQNSR 60
QY 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQILITPTE 120
Db 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQILITPTE 120
QY 121 DTEVGOALHSLINAAIMSVIWMITLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db 121 DTEVGOALHSLINAAIMSVIWMITLLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMALVFICY 240
Db 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMALVFICY 240
QY 241 LPEWTAMLIIVSVYDLVAVLCLKGRLMVLTAQERNETLFPALISSTWMLVNMAB 300
Db 241 LPEWTAMLIIVSVYDLVAVLCLKGRLMVLTAQERNETLFPALISSTWMLVNMAB 300
QY 301 GDEPAQRVSKNSKNAESTERESQDTVAENDGGESEWEAQRDHLGPHRSTPESRAA 360
Db 301 GDEPAQRVSKNSKNAESTERESQDTVAENDGGESEWEAQRDHLGPHRSTPESRAA 360

```

Db      301 GDEPQRRVSKNSKYNASTERESQDTVAENDDGGSEEMEAQORSHLGPFRSTPESRAA 360
Qy      361 VOELSSSIAGDEDEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
Db      361 VOELSSSIAGDEDEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
Qy      421 TLLLLAIFKKALPALPISITTFGLVFFAFADYLVQPMQDLAFHOFYI 467
Db      421 TLLLLAIFKKALPALPISITTFGLVFFAFADYLVQPMQDLAFHOFYI 467

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RESULT 8
US-10-221-254-4
; Sequence 4, Application US/10221254
; Publication No. US20030113811A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: PG3950USW
; CURRENT APPLICATION NUMBER: US/10/221,254
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0005894.1
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-254-4

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```

Query Match      99.5%; Score 2378; DB 14; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MTELPAPLSYFQNAQMSQEDNHLSTNTRSQNDNREROHNDRLSLGHPEPLSNGRPOGNSR 60
Db      1 MTELPAPLSYFQNAQMSQEDNHLSTNTRSQNDNREROHNDRLSLGHPEPLSNGRPOGNSR 60
Qy      61 QVVEODEEEDDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKDGOLITPTE 120
Db      61 QVVEODEEEDDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKDGOLITPTE 120
Qy      121 DTEVQGRALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db      121 DTEVQGRALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Qy      181 YLGEVFKTVNAVADYITVALLINFGVGMISIMKGPLRLQQAIVLIMISALMALVFIKY 240
Db      181 YLGEVFKTVNAVADYITVALLINFGVGMISIMKGPLRLQQAIVLIMISALMALVFIKY 240
Qy      241 LPBWTAMLLAVISYVDLVAVLCLKGPLRLMLVETAGERNETLFPALIVYSTWVLVYMAE 300
Db      241 LPBWTAMLLAVISYVDLVAVLCLKGPLRLMLVETAGERNETLFPALIVYSTWVLVYMAE 300
Qy      301 GDEPAQRVSKNSKYNASTERESQDTVAENDDGGSEEMEAQORSHLGPFRSTPESRAA 360
Db      301 GDEPAQRVSKNSKYNASTERESQDTVAENDDGGSEEMEAQORSHLGPFRSTPESRAA 360
Qy      361 VOELSSSIAGDEDEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
Db      361 VOELSSSIAGDEDEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
Qy      421 TLLLLAIFKKALPALPISITTFGLVFFAFADYLVQPMQDLAFHOFYI 467
Db      421 TLLLLAIFKKALPALPISITTFGLVFFAFADYLVQPMQDLAFHOFYI 467

```

```

RESULT 9
US-10-180-781-3
; Sequence 3, Application US/10180781
; Publication No. US20030150880A1

```

```

GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
            Schellenberg, Gerard D.
            Wasco, Wilma
            Levy-Lahad, Ephrat
            Bird, Thomas D.
            Galas, David J.

```

```

TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
ALZHEIMER'S DISEASE

```

```

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESS: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Ave, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/180,781
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 920010.571C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

```

```

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

```

```

US-10-180-781-3
Query Match      99.5%; Score 2378; DB 14; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MTELPAPLSYFQNAQMSQEDNHLSTNTRSQNDNREROHNDRLSLGHPEPLSNGRPOGNSR 60
Db      1 MTELPAPLSYFQNAQMSQEDNHLSTNTRSQNDNREROHNDRLSLGHPEPLSNGRPOGNSR 60
Qy      61 QVVEODEEEDDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKDGOLITPTE 120
Db      61 QVVEODEEEDDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKDGOLITPTE 120
Qy      121 DTEVQGRALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db      121 DTEVQGRALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
Qy      181 YLGEVFKTVNAVADYITVALLINFGVGMISIMKGPLRLQQAIVLIMISALMALVFIKY 240
Db      181 YLGEVFKTVNAVADYITVALLINFGVGMISIMKGPLRLQQAIVLIMISALMALVFIKY 240
Qy      241 LPBWTAMLLAVISYVDLVAVLCLKGPLRLMLVETAGERNETLFPALIVYSTWVLVYMAE 300
Db      241 LPBWTAMLLAVISYVDLVAVLCLKGPLRLMLVETAGERNETLFPALIVYSTWVLVYMAE 300
Qy      301 GDEPAQRVSKNSKYNASTERESQDTVAENDDGGSEEMEAQORSHLGPFRSTPESRAA 360
Db      301 GDEPAQRVSKNSKYNASTERESQDTVAENDDGGSEEMEAQORSHLGPFRSTPESRAA 360
Qy      361 VOELSSSIAGDEDEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
Db      361 VOELSSSIAGDEDEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420

```


QY 421 TLLLLAFKRLPALPISITGVLFPATDYLVOPEMDQLAFHOFYI 467
 Db 421 TLLLLAFKRLPALPISITGVLFPATDYLVOPEMDQLAFHOFYI 467

RESULT 10

US-10-417-422-4
 ; Sequence 4, Application US/10417422
 ; Publication No. US20030219720A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCARTHY, JUSTIN
 ; APPLICANT: CORDELL, BARBARA
 ; APPLICANT: SCIOS, INC.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
 ; TITLE OF INVENTION: NEURONAL DEGENERATION
 ; FILE REFERENCE: SCIOS.012C1
 ; CURRENT APPLICATION NUMBER: US/10/417.422
 ; CURRENT FILING DATE: 2003-04-14
 ; PRIOR APPLICATION NUMBER: 09/754949
 ; PRIOR FILING DATE: 2001-02-04
 ; PRIOR APPLICATION NUMBER: 60/175200
 ; PRIOR FILING DATE: 2000-01-10
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 467
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIEN
 US-10-417-422-4

Query Match 99.5%; Score 2378; DB 15; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2,2e-205;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNREROEHNDRRSLGHPPLSNRPOGNSR 60
 Db 1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNREROEHNDRRSLGHPPLSNRPOGNSR 60
 QY 61 QVEQDEDEDELTKYGAQVIMLFVPTLCMVVVAATIKSVSFYTRKDGQLIYTPFTE 120
 Db 61 QVEQDEDEDELTKYGAQVIMLFVPTLCMVVVAATIKSVSFYTRKDGQLIYTPFTE 120
 QY 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 QY 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 QY 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTIACFVAAILIGLCL 420
 Db 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTIACFVAAILIGLCL 420
 QY 421 TLLLLAFKRLPALPISITGVLFPATDYLVOPEMDQLAFHOFYI 467
 Db 421 TLLLLAFKRLPALPISITGVLFPATDYLVOPEMDQLAFHOFYI 467

RESULT 11
 US-09-785-474-4
 ; Sequence 4, Application US/09785474
 ; Patent No. US20010012626A1
 ; GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH
 ; MASCOT, WILMA
 ; TITLE OF INVENTION: Genetic Alterations Related To Familial
 ; Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/785,474
 ; FILING DATE: 20-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/706,344
 ; FILING DATE: 30-AUG-1996
 ; APPLICATION NUMBER: 60/003,054
 ; FILING DATE: 31-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KIM, JUDITH U.
 ; REGISTRATION NUMBER: 40,679
 ; REFERENCE/DOCKET NUMBER: 0609,4180002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 467 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-785-474-4
 Query Match 99.3%; Score 2374; DB 9; Length 467;
 Best Local Similarity 99.6%; Pred. No. 4.9e-205;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNREROEHNDRRSLGHPPLSNRPOGNSR 60
 Db 1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNREROEHNDRRSLGHPPLSNRPOGNSR 60
 QY 61 QVEQDEDEDELTKYGAQVIMLFVPTLCMVVVAATIKSVSFYTRKDGQLIYTPFTE 120
 Db 61 QVEQDEDEDELTKYGAQVIMLFVPTLCMVVVAATIKSVSFYTRKDGQLIYTPFTE 120
 QY 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 QY 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAIMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 QY 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDVAALCPKGPLRLMVEIAOERNETLFPALISSSTMWLVNMAE 300
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPBRSTPESRAA 360
 QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTIACFVAAILIGLCL 420
 Db 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTIACFVAAILIGLCL 420

QY 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQALPHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQALPHQFYI 467

RESULT 12

US-09-785-474-28
 Sequence 28, Application US/09785474
 Patent No. US20010012626A1
 GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/785,474

FILING DATE: 20-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,344

FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609.4180002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-785-474-28

Query Match 99.2%; Score 2372; DB 9; Length 467;

Best Local Similarity 99.6%; Pred. No. 7.5e-205;

Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 QY 61 QVEODEEEDBELTLKYGAKHYIMLFVPVTLQMVVVAATIKSVSFYTRKDGQLIYTPETE 120
 DB 61 QVEODEEEDBELTLKYGAKHYIMLFVPVTLQMVVVAATIKSVSFYTRKDGQLIYTPETE 120
 QY 121 DTEITGQALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 DB 121 DTEITGQALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240

QY 241 LPEWTAMLLIAVISYDVAVLCLKGPLRLVETARQENETLFPALITYSTMTWLVNMAE 300
 DB 241 LPEWTAMLLIAVISYDVAVLCLKGPLRLVETARQENETLFPALITYSTMTWLVNMAE 300
 QY 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSIILAGEDEEERGVKLGDFIFYSVLVKGASATASGDMNTTIAQFVALILGLCL 420
 DB 361 VOELSSSIILAGEDEEERGVKLGDFIFYSVLVKGASATASGDMNTTIAQFVALILGLCL 420
 QY 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQALPHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQALPHQFYI 467

RESULT 13

US-09-895-035-12

Sequence 12, Application US/09895035

Patent No. US20020082211A1

GENERAL INFORMATION:

APPLICANT: Patterson, Chandra

APPLICANT: Murty, Lynn E.

TITLE OF INVENTION: HUMAN PRESENTINILIN VARIANT

FILE REFERENCE: PC-0047 CIP

CURRENT APPLICATION NUMBER: US/09/895,035

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/116,640

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Perl Program

SEQ ID NO 12

LENGTH: 463

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20020082211A1 g1244638

US-09-895-035-12

Query Match 98.2%; Score 2348; DB 9; Length 463;

Best Local Similarity 98.7%; Pred. No. 1.1e-202;

Matches 461; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 QY 61 QVEODEEEDBELTLKYGAKHYIMLFVPVTLQMVVVAATIKSVSFYTRKDGQLIYTPETE 120
 DB 61 QVEODEEEDBELTLKYGAKHYIMLFVPVTLQMVVVAATIKSVSFYTRKDGQLIYTPETE 120
 QY 121 DTEITGQALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 DB 121 DTEITGQALSHSLNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIWNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPEWTAMLLIAVISYDVAVLCLKGPLRLVETARQENETLFPALITYSTMTWLVNMAE 300
 DB 241 LPEWTAMLLIAVISYDVAVLCLKGPLRLVETARQENETLFPALITYSTMTWLVNMAE 300
 QY 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSIILAGEDEEERGVKLGDFIFYSVLVKGASATASGDMNTTIAQFVALILGLCL 420
 DB 361 VOELSSSIILAGEDEEERGVKLGDFIFYSVLVKGASATASGDMNTTIAQFVALILGLCL 420

QY 421 TLLLAIFKALPALPISITGVLVFPATDYLVOPEMDQAFHQFYI 467
 DB 417 TLLLAIFKALPALPISITGVLVFPATDYLVOPEMDQAFHQFYI 463

RESULT 14

US-10-293-000-5
 ; Sequence 5, Application US/10293000
 ; Publication No. US20030175278A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monteiro, Meryn J.
 ; APPLICANT: Mah, Alex L.
 ; APPLICANT: Perry, George
 ; TITLE OF INVENTION: UBIQUILIN, A PRESENTILIN INTERACTOR AND METHODS OF USING SAME
 ; FILE REFERENCE: 4115-175
 ; CURRENT APPLICATION NUMBER: US/10/293,000
 ; CURRENT FILING DATE: 2003-04-01
 ; PRIOR APPLICATION NUMBER: US 60/338,549
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 467
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-293-000-5

Query Match 94.8%; Score 2266; DB 14; Length 467;
 Best Local Similarity 94.6%; Pred. No. 2,66-195;
 Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTELPAPISYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRRSLGHPPELSNGRPGNSR 60
 DB 1 MTELPAPISYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRRSLGHPPELSNGRPGNSG 60
 QY 61 QVDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSEFYTRKQGLIYPTFE 120
 DB 61 PVERDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSEFYTRKQGLIYPTFE 120
 QY 121 DTEVGRALHSILNAAIMISIVVMTLLVLYKYCYKVIHAMLIISLLFFPSFI 180
 DB 121 DTEVGRALHSILNAAIMISIVVMTLLVLYKYCYKVIHAMLIISLLFFPSFI 180
 QY 181 YLGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPWTAMLLIAVISYDVAVLCCKGPLRMLVETAQERNETLFPALIISSSTMVLVMAE 300
 DB 241 LPWTAMLLIAVISYDVAVLCCKGPLRMLVETAQERNETLFPALIISSSTMVLVMAE 300
 QY 301 GDPPEQRVSKSKNAESTERESODTYAENDDGGFSEEMEAQRDSDLGPHRSTPESRAA 360
 DB 301 GDPPEQRVSKSKNAESTERESODTYAENDDGGFSEEMEAQRDSDLGPHRSTPESRAA 360
 QY 361 VQESSIILAGEDEPEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCT 420
 DB 361 VQESSIILAGEDEPEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCT 420
 QY 421 TLLLAIFKALPALPISITGVLVFPATDYLVOPEMDQAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITGVLVFPATDYLVOPEMDQAFHQFYI 467

RESULT 15

US-09-878-454A-1
 ; Sequence 1, Application US/09878454A
 ; Patent No. US20020064828A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monteiro, et al.
 ; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentilin

FILE REFERENCE: 4115-161
 ; CURRENT APPLICATION NUMBER: US/09/878,454A
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: 60/210,939
 ; PRIOR FILING DATE: 2000-06-11
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-878-454A-1

Query Match 60.7%; Score 1452; DB 9; Length 448;
 Best Local Similarity 65.2%; Pred. No. 5e-122;
 Matches 304; Conservative 40; Mismatches 80; Indels 42; Gaps 8;

QY 3 ELPLPAPISYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRRSLGHPPELSNGRPGNSRQ 61
 DB 24 EBPTRSCQEGRGDEDENTAOMRSQNEDEDEDPDRYQSGVF-----GRPG----- 74
 QY 62 VVEODEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSEFYTRKQGLIYPTFE 121
 DB 75 -----LEELTKYGAHVIMLFVPTLCMVVVVATIKSVSEFYTRKQGLIYPTFE 127
 QY 122 TETVGRALHSILNAAIMISIVVMTLLVLYKYCYKVIHAMLIISLLFFPSFIY 181
 DB 128 TSVGQRLNLSYVNTLIMISIVVMTLLVLYKYCYKVIHAMLIISLLFFPSFIY 187
 QY 182 LGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 241
 DB 188 LGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 247
 QY 242 LPWTAMLLIAVISYDVAVLCCKGPLRMLVETAQERNETLFPALIISSSTMVLVMAE 301
 DB 248 PMSAMVILGASVYDVAVLCCKGPLRMLVETAQERNETLFPALIISSSAMVILGMAK 307
 QY 302 DEAPQRVSKSKNAESTERESODTYAENDDGGFSEEMEAQRDSDLGPHRSTPESRAA 361
 DB 308 DSSQAL--QVYDPE--NEEDSYDSFGE--PSYFVFPPEPLTGPB----- 349
 QY 362 QELSSIILAGEDEPEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCT 421
 DB 350 BEL-----EEERGVKLGDFIFYSVLVGKAAAGSGDMNTTIACFVALIIGLCT 402
 QY 422 TLLLAIFKALPALPISITGVLVFPATDYLVOPEMDQAFHQFYI 467
 DB 403 TLLLAIFKALPALPISITGVLVFPATDYLVOPEMDQAFHQFYI 448

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 Job time : 49 secs